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(54) Title: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.



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GENE EXPRESSION PROFILING OF PRIMARY BREAST
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

5 This invention relates to polynucleotide analysis
and, in particular, to polynucleotide expression profiling of
carcinomas using arrays of candidate polynucleotides.

10 Pathologists and clinicians in charge of the
management of breast cancer patients are facing two major
problems, namely the extensive heterogeneity of the disease
and the lack of factors - among conventional histological and
clinical features - predicting with reliability the evolution
of the disease and its sensitivity to cancer therapies.
Breast tumors of the same apparent prognostic type vary
widely in their responsiveness to therapy and consequent
15 survival of the patient. New prognostic and predictive
factors are needed to allow an individualization of therapy
for each patient.

20 Great hope is currently being placed on molecular
studies, which address the problem in a global fashion.
Methods such as cytogenetics, comparative genomic
hybridization, and whole-genome allelotyping have addressed
the issue at the genome level. Currently, the modifications
that take place in human tumors at the level of transcription
can also be studied in a large, unprecedented scale, using
25 new methods such as cDNA arrays that allow quantitative
measurement of the mRNA expression levels of many genes
simultaneously. Thus, it would be advantageous to provide a
means to assess the capacity of cDNA array testing in
clinical practice to better classify an heterogeneous cancer
30 into tumor subtypes with more homogeneous clinical outcomes,
and to identify new potential prognostic factors and
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ($p \leq 0.0001$) and that of GATA3 with the presence of estrogen receptors ($p \leq 0.001$). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA

array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can
15 range from hundreds to thousands.

DNA microarrays have serve a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex); wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.

The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

- a) obtaining a polynucleotide sample from a patient; and
- 5 b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
- 10 libraries and
- c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences

15 of the invention wherein the amount of reaction product of step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by

20 reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step (b) comprises a hybridization of the sample RNA with the labeled probe.

25 The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30 The method for detecting differentially expressed polynucleotide sequences is particular useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

5 The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

10 Le label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

15 The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation
20 table 10 allows to identify these sequences in the sequence listing of the present application in annex).

 In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ;
25 SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ;
SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ;
SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No : 63 ;
SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No : 87 ;
SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID
30 No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ;
SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No : 116 ;
SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ ID No : 139 ;
SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ; SEQ ID No : 151 ;
SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 5 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex),
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6
in priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex), which distinguish a healthy
person from a person with cancer.

20 In another particular embodiment the invention relates
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 7 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex)
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5 In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;
SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14
10 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID
No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;
15 SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these
SEQ ID N° refer to old SEQ ID N° presented on table 11 in
priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex) which distinguish tumors
20 sensitive to anthracycline from tumors unsensitive to
anthracycline.

 The invention relates also to a method of detecting
differentially expressed genes correlated with a cancer
25 comprising detecting at least one library of polynucleotide
sequences as above defined or of products encoded by said
library in a sample obtained from a patient.

 A particular embodiment of the invention relates
30 to a polynucleotide library of corresponding substantially to
any combination of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets 1 to set 212 as defined in
table 4

The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from anthracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an anthracycline-sensitive tumor from patients having an anthracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination
20 of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in
25 table 6B.

The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at
30 least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

In a particular embodiment the reaction product of step (c) is quantified by further comparison of said reaction product to a control sample.

5 In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

10 Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

15 Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

20 This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

25 The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

30 The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJI BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>). Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a LaPlacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software. Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were measured with the correlation coefficient r . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

Northern blot analysis

Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a α -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5 μ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF α 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples (n = 35) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones (n = 162) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.

The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ($p < 0.005$, log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ($p < 0.05$, log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ($p = 0.0004$). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and α -actin (bottom). ER status is indicated for each tumor sample.

Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a
15 tissue sample and each row to a gene. For graphic purposes, genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to
20 expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values
25 is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than
30 the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A ($n = 15$, including normal breast, NB) and B ($n = 20$). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 ($n = 6$) and A2 ($n = 6$), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ($p = 0.01$) and overall survival ($p = 0.005$) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1						A2					
Tumor position in the cluster	1	2	3	4	5	6	7	8	9	10	11	12
Age, years	46	58	60	63	51	58	46	47	50	47	46	66
Nodal status	1	0	0	16	13	37	10	4	1	2	0	0
Histological size, mm	60	20	26	35	20	30	27	25	30	25	20	22
SBR grade												
ER status	neg	neg	neg	neg	neg	neg	pos	neg	pos	pos	pos	pos
Adjuvant chemotherapy	yes	yes	no	yes	yes	yes	yes	yes	no	yes	no	no
Metastasis	yes	no	yes	yes	no	yes	no	no	no	no	no	no
Follow-up, months	58	106	35	47	41	31	85	98	95	49	19	141
Patient status	D	A	D	D	A	D	A	A	A	A	A	A

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

TABLE 2

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFBR3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XBP1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ($r = 0.68$; $p \leq 0.0001$).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ($r = 0.91$; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5 Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

Gene expression profiles were able to make this
25 discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5 Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating rate, favorable prognosis and response to hormonal therapy. 10 The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes 15 could serve as predictive factors to guide the therapy.

GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other 20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in 25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high 30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the

possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5 Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a series of poor prognosis breast tumors, two subtypes of the
10 disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15 Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,
20 and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3 '	Seq5 '	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST RS5460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3 '	Seq5 '	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hnrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC13071	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

TABLE 5B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

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Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples.

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TABLE 6

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XPB1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

Table 6A
overexpressed genes : top 5
ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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Table 6B
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7A

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

TABLE 7B

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to anthracycline from tumors unsensitive to anthracycline.

TABLE 8

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating (hepatocyte growth factor-like) 1	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to anthracycline from tumors unsensitive to anthracycline.

TABLEAU 8A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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TABLEAU 8B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 e1a binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9A

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5 Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMY3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP-11) (ex STMY3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (Li-Fraumeni syndrome) (TP53)	205314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	126233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (TIT3 complex) (CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRY (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topoIIb mRNA for topoisomerase IIb.	130798		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	246620	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase pi (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDNP2	19	ectonucleotide pyrophosphatase/phosphodiesterase 2(autotaxin) (ENPP2) (ex PDNP2)	120916	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selectin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ERBB2	24	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	179197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol Ttk2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p60, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T85683	40	EST T85683 cathepsin B (CTSB)	112622		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFBR3	42	transforming growth factor, beta receptor III (TGFBR3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110599	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180219	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192688		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	156979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EPHA2	52	Epha2 (EPHA2)	162004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	cAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MX1)	298242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	(POU2F2)	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	139326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	309943	SEQ ID No : 99		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
RIL	66	LM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R97218	69	Est R97218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:88	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p66shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141924		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	196282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3 ' US PROV LISTING	Seq5 ' US PROV LISTING	Seq3 ' PCT Listing	Seq5 ' PCT Listing	(mRNA) PCT Listing
TNXA	87	tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251963	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204586	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37)	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	162997		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
APC	93	adenomatosis polyposis coli (APC)	125294	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopachrome tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast) homolog 1 (ATOX1) (ex EMS1)	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit,	182610	SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No : 164	0	SEQ ID No:208	SEQ ID No:209
ANXA11	110	annexin A11 (ANXA11)	158892		SEQ ID No : 165	0	SEQ ID No:206	SEQ ID No:207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	159809		SEQ ID No : 166	0	SEQ ID No:212	SEQ ID No:213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	153974	SEQ ID No : 167	SEQ ID No : 168	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
BTF3L3	113	basic transcription factor 3 (BTF3)	195889	SEQ ID No : 169		SEQ ID No:289	0	SEQ ID No:290
EST R55460	114	EST R55460	154997		SEQ ID No : 170	0	SEQ ID No:185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No : 171		SEQ ID No:253	0	SEQ ID No:254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No : 172	SEQ ID No : 173	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit.alpha isoform (PPP2CA)	154685	SEQ ID No : 174	SEQ ID No : 175	0	SEQ ID No:183	SEQ ID No:184
MDM2	118	mouse double minute 2, human homolog of p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No : 176		0	SEQ ID No:120	SEQ ID No:121
TNFRSF6	119	tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	151767	SEQ ID No : 177	SEQ ID No : 178	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CNTFR	120	ciliary neurotrophic factor receptor (CNTFR)	156431		SEQ ID No : 179	0	SEQ ID No:192	SEQ ID No:193
JUNB	121	jun B proto-oncogene (JUNB)	153213	SEQ ID No : 180	SEQ ID No : 181	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CCND1	122	cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No : 182		SEQ ID No:9	0	SEQ ID No:10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No : 183	SEQ ID No : 184	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130323	SEQ ID No : 185	SEQ ID No : 186	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210874	SEQ ID No : 187	SEQ ID No : 188	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
TIMP1	126	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP-1)	162246	SEQ ID No : 189	SEQ ID No : 190	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
YES1	127	y-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No : 191		SEQ ID No:303	0	SEQ ID No:304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No : 192	0	SEQ ID No:25	SEQ ID No:26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No : 193	0	SEQ ID No:263	SEQ ID No:264

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathepsin D (lysosomal aspartyl protease) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	188380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847	SEQ ID No : 197		SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	Integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363796	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300564	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELa)	122056	SEQ ID No : 212		SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (calgizzarin) (S100A11)	155345	SEQ ID No : 213	SEQ ID No : 214	SEQ ID No:186	0	0
ANG	142	angiogenin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 215	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	Integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 216	SEQ ID No : 217	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 (HRMT1L1) (ex PRMT2)	158038	SEQ ID No : 218	SEQ ID No : 219	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55460	145	EST R55460	154997		SEQ ID No : 220	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 221	SEQ ID No : 222	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9)	323948	SEQ ID No : 223		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329		SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4) (TFAP4)						
ELF1	152	Human cis-acting sequence. Elf-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120649	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	interleukin 3 receptor (hIL-3Ra)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	junction plakoglobin (JUP)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	160764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:436	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	162499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 Precursor = LACTOGEN	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine protein kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST AW184517	rien		image ?					

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CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74; SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET 34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:78) ; SET 42: (SEQ ID No:102; SEQ ID No:103) ; SET 43: (SEQ ID No:104; SEQ ID No:105) ; SET 44: (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET 45: (SEQ ID No:109; SEQ ID No:110) ; SET 46: (SEQ ID No:111; SEQ ID No:112; SEQ ID No:113) ; SET 47: (SEQ ID No:114) ; SET 48: (SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET 49: (SEQ ID No:118; SEQ ID No:119) ; SET 50: (SEQ ID No:120; SEQ ID No:121) ; SET 51: (SEQ ID No:122; SEQ ID No:78) ; SET 52: (SEQ ID No:123; SEQ ID No:124; SEQ ID No:125) ; SET 53: (SEQ ID No:126; SEQ ID No:127; SEQ ID No:128) ; SET 54: (SEQ ID No:129; SEQ ID No:130) ; SET 55: (SEQ ID No:131; SEQ ID No:132) ; SET 56: (SEQ ID No:133; SEQ ID No:134) ; SET 57: (SEQ ID No:135; SEQ ID No:136; SEQ ID No:137) ; SET 58: (SEQ ID No:138; SEQ ID No:139; SEQ ID No:140) ; SET 59: (SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ; SET 60: (SEQ ID No:144; SEQ ID No:145; SEQ ID No:146) ; SET 61: (SEQ ID No:147; SEQ ID No:148; SEQ ID No:149) ; SET 62: (SEQ ID No:150; SEQ ID No:151; SEQ ID No:152) ; SET 63: (SEQ ID No:153; SEQ ID No:154; SEQ ID No:155) ; SET 64: (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET 65: (SEQ ID No:159; SEQ ID No:160; SEQ ID No:161) ; SET 66: (SEQ ID No:162; SEQ ID No:163) ; SET 67: (SEQ ID No:164; SEQ ID No:165) ; SET 68: (SEQ ID No:166; SEQ ID No:167; SEQ ID No:152) ; SET 69: (SEQ ID No:168; SEQ ID No:169; SEQ ID No:170) ; SET 70: (SEQ ID No:171; SEQ ID No:172) ; SET 71: (SEQ ID No:173; SEQ ID No:174; SEQ ID No:175) ; SET 72: (SEQ ID No:176; SEQ ID No:177) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 74: (SEQ ID No:180; SEQ ID No:181; SEQ ID No:182) ; SET 75: (SEQ ID No:183; SEQ ID No:184) ; SET 76: (SEQ ID No:185) ; SET 77: (SEQ ID No:186) ; SET 78: (SEQ ID No:187; SEQ ID No:188) ; SET 79: (SEQ ID No:189;

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199; SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ; SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212; SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ; SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95: (SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ; SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248; SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ; SET 110: (SEQ ID No:262; SEQ ID No:200) ; SET 111: (SEQ ID No:263; SEQ ID No:264) ; SET 112: (SEQ ID No:265; SEQ ID No:266) ; SET 113: (SEQ ID No:267; SEQ ID No:268) ; SET 114: (SEQ ID No:269; SEQ ID No:270) ; SET 115: (SEQ ID No:271; SEQ ID No:272) ; SET 116: (SEQ ID No:273; SEQ ID No:274) ; SET 117: (SEQ ID No:275; SEQ ID No:276) ; SET 118: (SEQ ID No:277; SEQ ID No:278) ; SET 119: (SEQ ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 120: (SEQ ID No:282; SEQ ID No:283; SEQ ID No:276) ; SET 121: (SEQ ID No:284; SEQ ID No:285) ; SET 122: (SEQ ID No:286; SEQ ID No:287; SEQ ID No:288) ; SET 123: (SEQ ID No:289; SEQ ID No:290) ; SET 124: (SEQ ID No:291; SEQ ID No:292) ; SET 125: (SEQ ID No:293; SEQ ID No:294; SEQ ID No:295) ; SET 126: (SEQ ID No:296; SEQ ID No:297) ; SET 127: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 128: (SEQ ID No:301; SEQ ID No:302; SEQ ID No:288) ; SET 129: (SEQ ID No:303; SEQ ID No:304) ; SET 130: (SEQ ID No:305; SEQ ID No:306;

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ; SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134: (SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ; SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326; SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142: (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ; SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET 150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31) ; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET 154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382; SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389; SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ; SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404; SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450): SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:
(SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID
10 No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ
ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID
15 No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET
147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;
20 SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim
4 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

6. A polynucleotide library according to Claim 4
35 wherein the pool of polynucleotide sequences or subsequences

correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) and SET 181: (SEQ ID No:431)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID No:432).

7 A polynucleotide library according to Claim 6 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

8. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32: (SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET 107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),

wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID
No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ
ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;
10 SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID
No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID
15 No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

 wherein said sequences are useful in
differentiating antracycline-sensitive tumors from
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim
16 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

18. A library according to Claim 16 wherein the
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No 174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

19. A polynucleotide library according to Claim 18 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

20. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23 (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ; SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39 (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ; SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96 (SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258) ; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276) ; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296; SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344) ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108) ; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166 (SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401) ; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424; SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184 (SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

wherein said sequences are useful in classifying good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim 20 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID

No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the
15 genes identified by said first group of cluster sequences
with the underexpression of the genes identified by said
second group of cluster sequences are useful in classifying
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim
22 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
25 predefined sets.

24. A polynucleotide library according to anyone
of Claims 1 to 23 wherein said tumor cells are breast tumor
cells.

30 25. A polynucleotide library according to any of
Claims 1 to 23 wherein said polynucleotides are immobilized
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

5 33. A method of detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

20 34. A method for detecting differentially expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

25 35. A method for detecting differentially expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5 37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10 38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15 39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20 40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25 41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30 42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequences sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

5

Figure 1

Normal Breast

Figure 1A

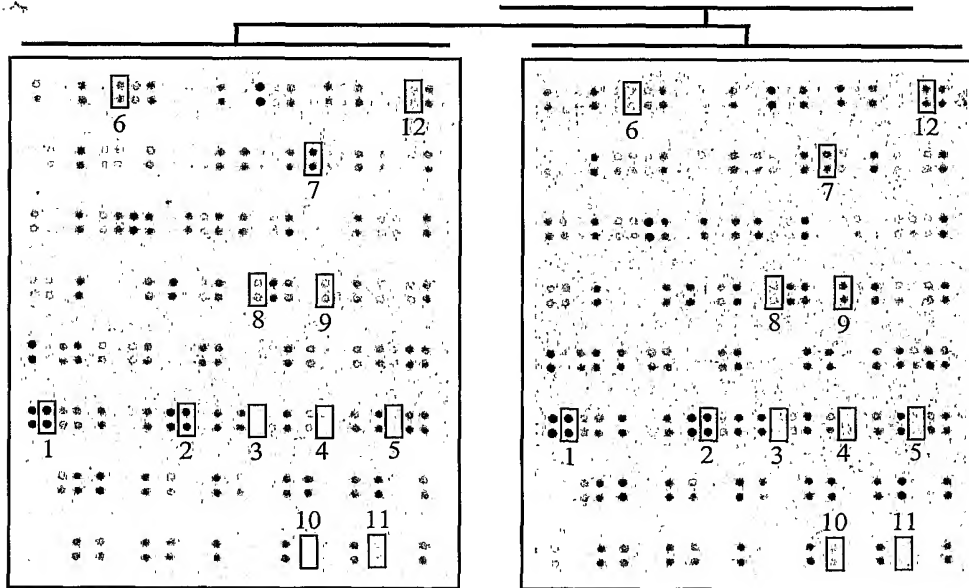
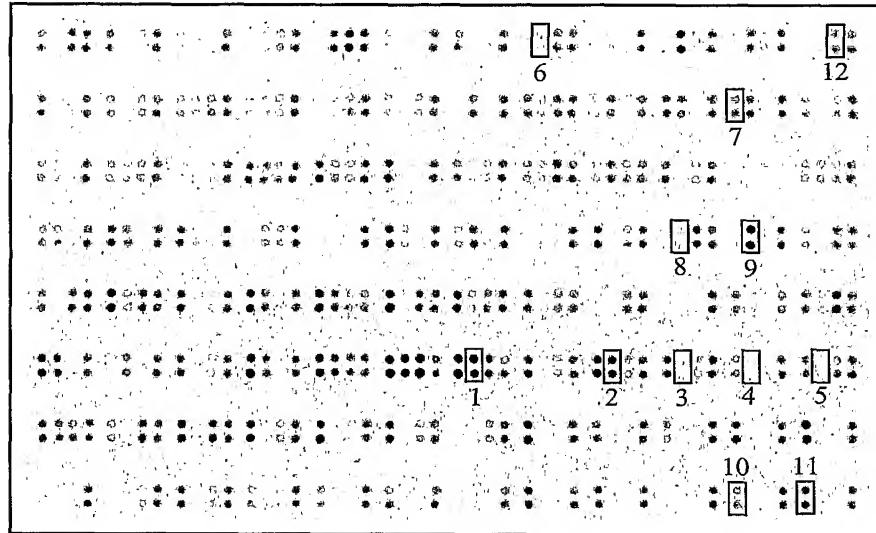


Figure 1B

ER-

ER+

Figure 1C

Breast cancer

Figure 2

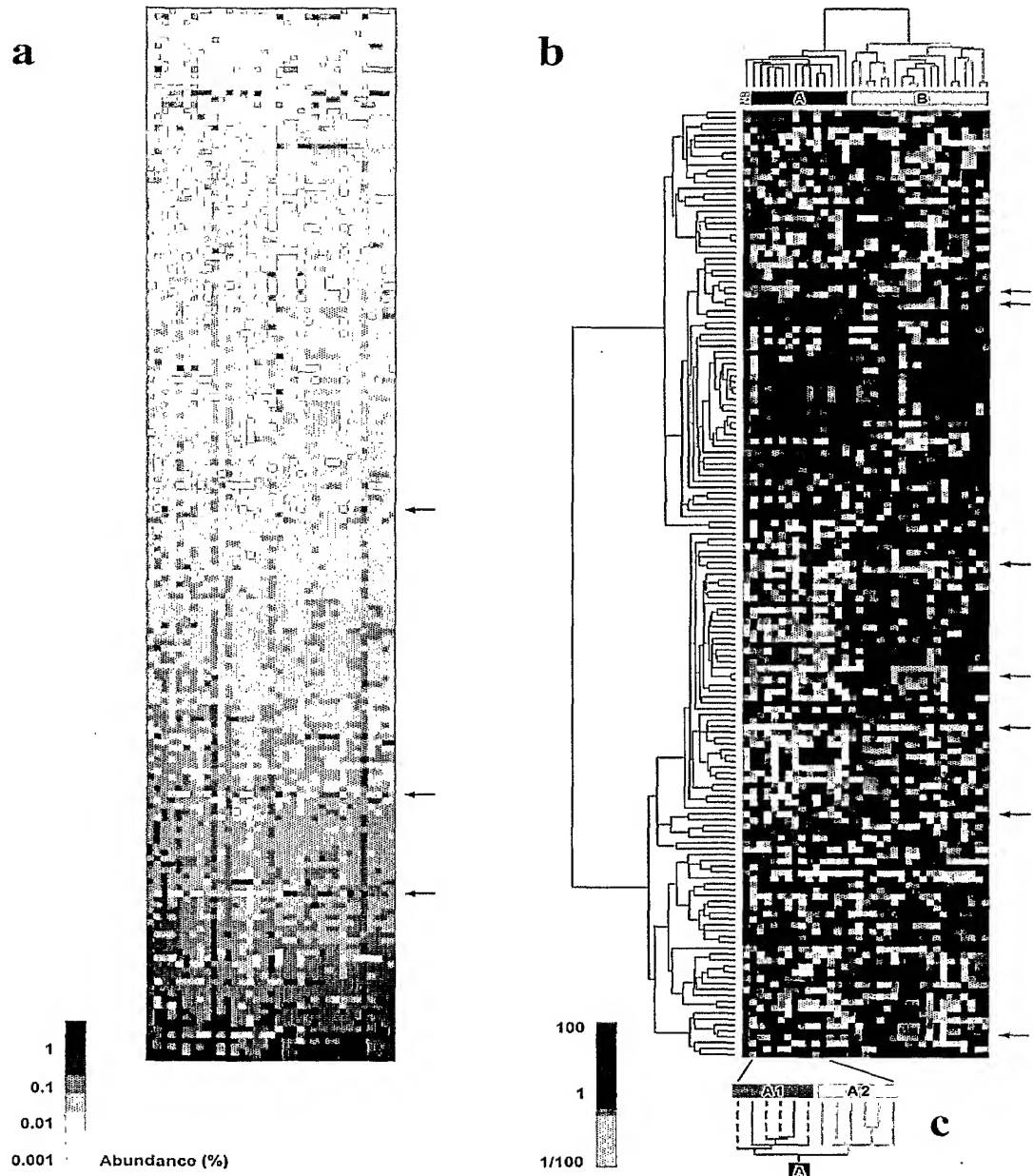


Figure 3

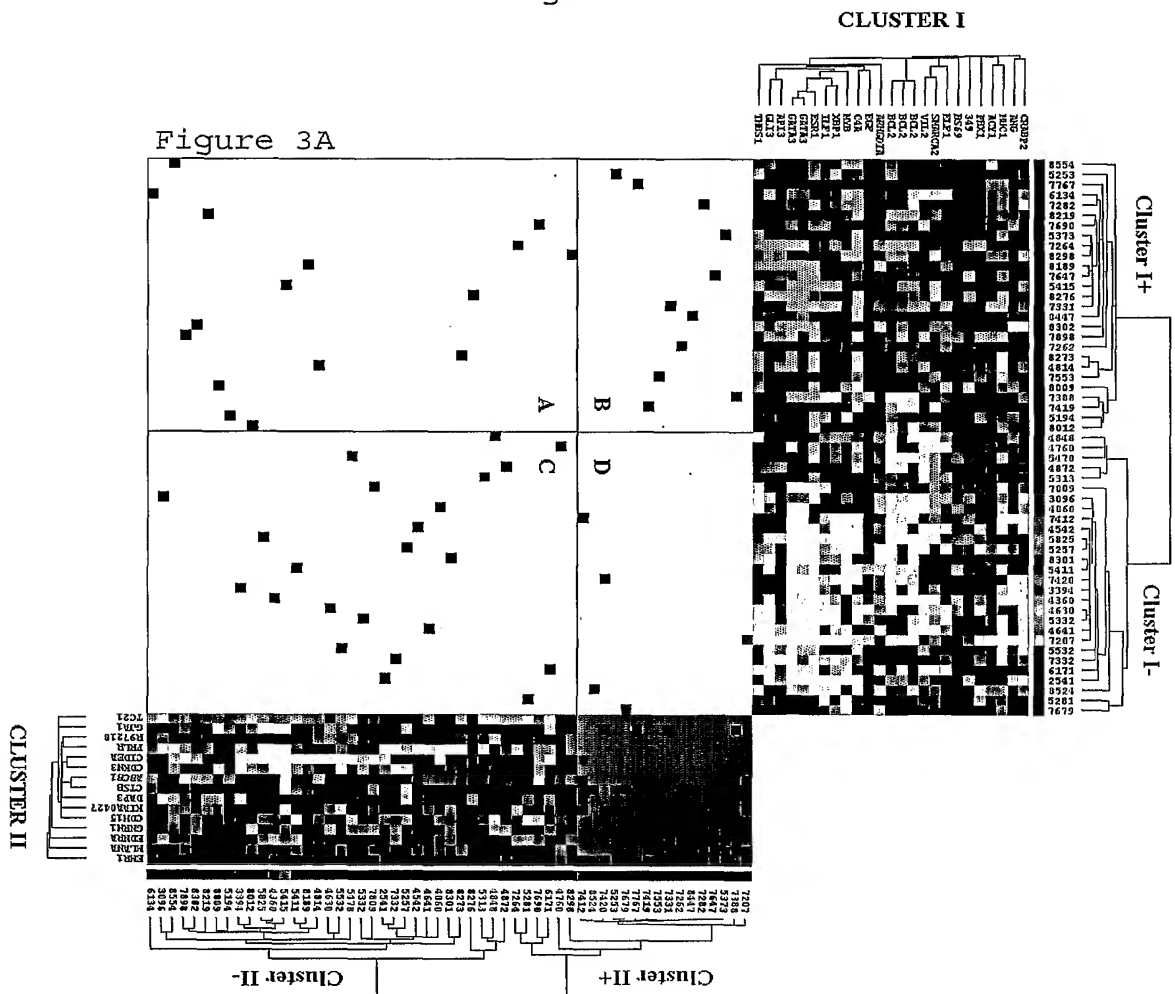


Figure 3C

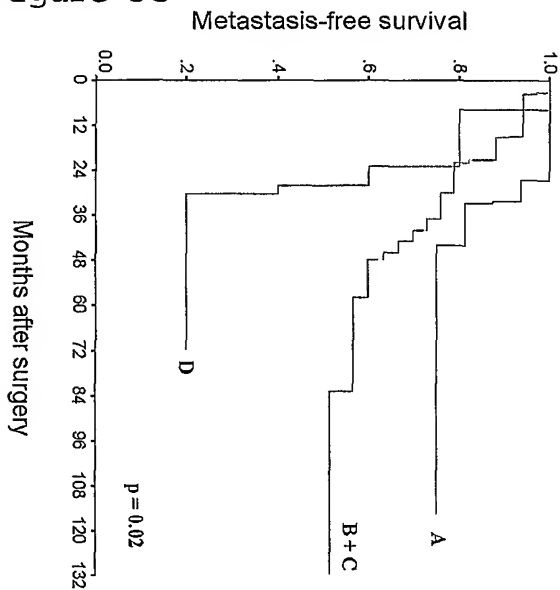


Figure 3B

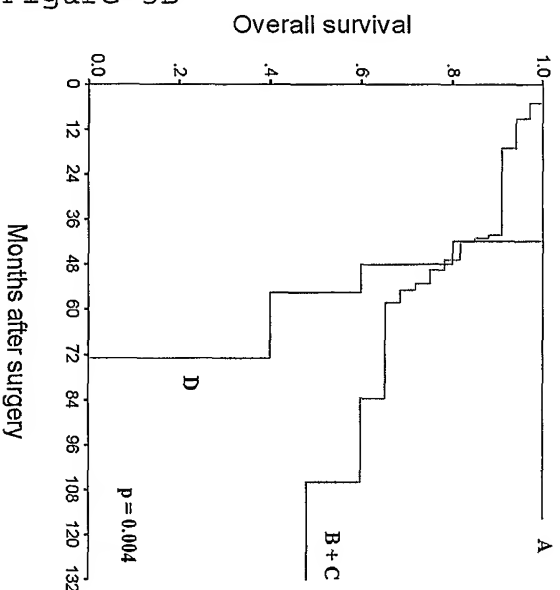


Figure 4

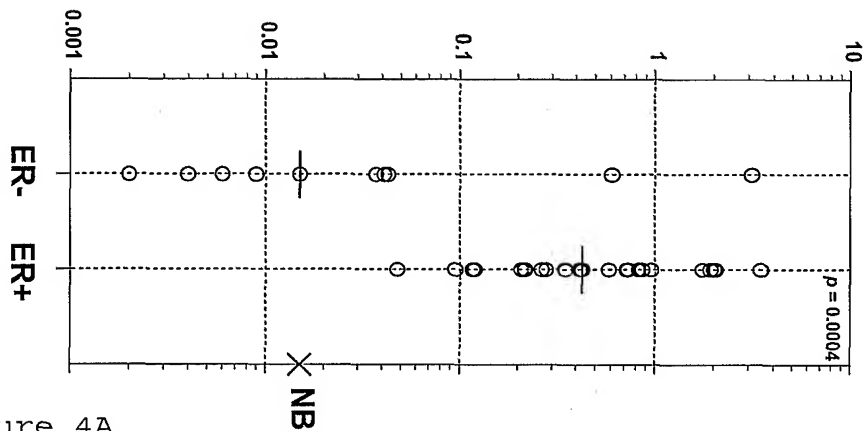


Figure 4A

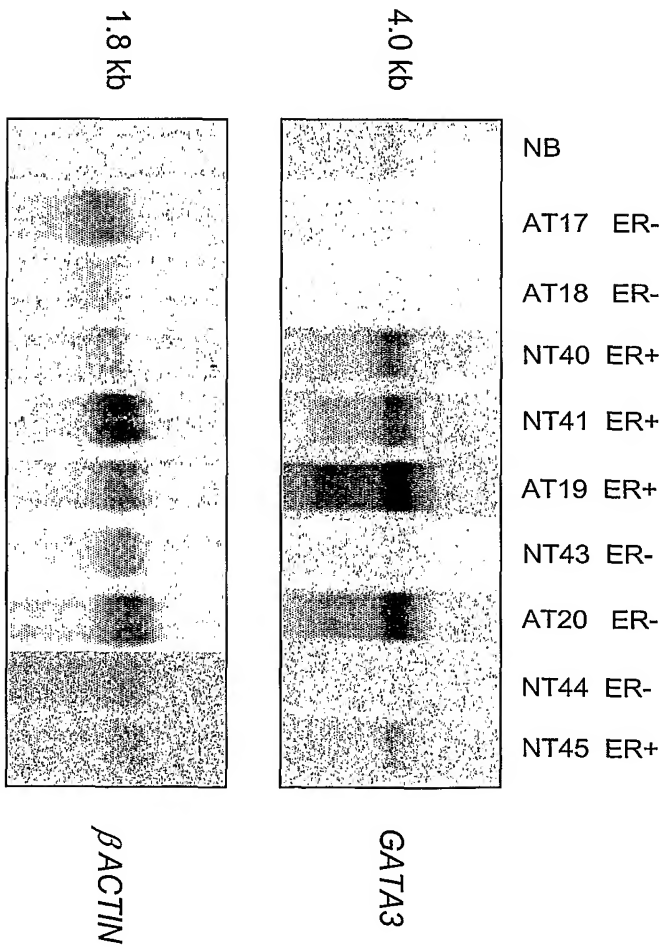


Figure 4B

SEQUENCE LISTING

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<110> François Bertucci
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Catherine Nguyen
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 <222> (1)..(3327)
 <223> tousled-like kinase 2 (TLK2) gene.

<400> 6
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 ggagagcgga gctccgcagc cgggtcgggt cggggccctt cccgggagga gcgtaggagc 120
 cggcggcggc ggcggcagca gaaatgatgg aagaattgca tagcctggac ccacgcagg c 180
 aggaattatt ggaggccagg tttactggag taggtgttag taagggacca cttaatagt 240
 agtcttccaa ccagagcttg tgcagcgtcg gatccttgag tgataaagaa gtagagactc 300
 ccgagaaaaa gcagaatgac cagcgaaatc ggaaaagaaa agctgaacca tatgaaacta 360
 gccaaaggga aggcactcct aggggacata aaattag tga ttacttttag tttgctgggg 420
 gaagcgcgcc aggaaccagc cctggcagaa gtgttccacc agttgcacga tcctcaccgc 480
 aacattcctt atccaatccc ttaccgcgac gactagaaca gccctctat ggttttagatg 540
 gcagtgtctg aaaggaggca acggaggagc agtctgctct gccaacctc atgtcagtga 600
 tgctagcaaa acctcggctt gacacagagc agctggcgca aaggggagct ggcctctgct 660
 tcacttttgt ttcagctcag caaaacagtc cctcatctac gggatctggc aacacagagc 720
 attcctgcag ctcccaaaaa cagatctcca tcacgcacag acggaccag tccgacctca 780
 caatagaaaa aatatctgca ctagaaaaa gtaagaattc tgacttagag aagaagg agg 840
 gaagaataga tgatttatta agagccaact gtgatttgag acggcagatt gatgaacagc 900
 aaaagatgct agagaaatac aaggaaacgat taaatagatg tgtgacaatg agcaagaaac 960
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 gcttgagact gggccacttt actactgtcc gaca cggagc ctcatctact gaacagtga 1080
 cagatggtta tgcttttcag aatcttatca agcaacagga aaggataaat tcacagaggg 1140
 aagagataga aagacaacgg aaaatgttag caaagcggaa acctcctgcc atgggtcagg 1200
 cccctcctgc aaccaatgag cagaaaacagc ggaaaagcaa gaccaatgga gctgaaaaatg 1260
 aaacgttaac gtttagcagaa taccatgaac aagaagaaat cttcaaactc agattaggtc 1320
 atcttaaaaa ggaggaagca gagatccagg cagagctgga gagactagaa agggttagaa 1380

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atctacatat caggggaacta aaaaggatac ataatgaaga taattcacaa tttaaagatc 1440
atccaacgct aaatgacaga tatttggtgt tacatctttt gggtagag ga ggtttcagtg 1500
aagtttacaa ggcatttgat ctaacagagc aaagatacgt agctgtgaaa attcaccagt 1560
taaataaaaa ctggagagat gagaaaaagg agaattacca caagcatgca tgtagggaat 1620
accggattca taaagagctg gatcatccca gaatagttaa gctgtatgat tacttttcac 1680
tggatactga ctcgttttgt ac agtattag aatactgtga gggaaatgat ctggacttct 1740
acctgaaaac gcacaaatta atgtcggaga aagaggcccg gtccattatc atgcagattg 1800
tgaatgcttt aaagtactta aatgaaataa aacctcccat catacactat gacctcaaac 1860
caggtaatat tcttttagta aatggtacag cgtgtggaga gataaaaaatt acagattttg 1 920
gtctttcgaa gatcatggat gatgatagct acaattcagt ggatggcatg gagctaacat 1980
cacaaggtgc tgggtacttat tgggtatttac caccagagtg ttttgtggtt gggaaagaac 2040
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tttatggaag gaagcctttt ggccataacc agtctc agca agacatccta caagagaata 2160
cgattcttaa agctactgaa gtgcagttcc cgccaaagcc agtagtaaca cctgaagcaa 2220
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tggcctgtga tccctacttg ttgcctcaca tccgaaagtc agtctctaca agtagccctg 2340
ctggagctgc tattgcatca acctctgggg cgtccaataa cagttcttct aattgagact 2400
gactccaagg ccacaaactg ttcaacacac acaaagtggg caaatggcgt tcagcagcgg 2460
gtttggaaca tagcgaatcc gaatggatct gatgaaacct gtaccaggtg cttttatttt 2520
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ggcagctccg gccaggcctt gtaggaaaaa gccccgccc aggttccagc gtcaacggcc 2640
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tcattccaat cagatgcagc tttctctctc gtctggtctc ctgtttgcaa ttgcttccct 3120
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caaagaatga ggtagaaga ctgcagcttg gagtctct ct aggttttcaa ctatttcttc 3240
acaatttgaa cacttgacgg ttgtcccttt taatttattt gaagtgcctat ttttttaaat 3300
aaaggttcat ctgtccatgc aaaaaaa 3327

```

<210> 7

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(300)

<223> 3' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 7

```

tncaagagac aggggttnngc acattgcccc ggatgggtctc aaactcctag agttgagcta 60
tccaccacc tttggcctnc caaagtgtct ggatcacagg cgtgagtcac tgtntccagc 120
accatcttg aggtctctta aagcccaggc cccacgccga gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctc ctgctggtcc aggggcccc 240
ctttgaagaa ccactgcact gggtntttcc tctgggaccc gaatgcctgt gcttctcccc 300

```

<210> 8

<211> 369

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(369)
<223> 5' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 8
cctaacgcag gtttccccgc aaatgactgg tcacgcggga ctgaacaccg cacaggcagg 60
aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttcctaccta accgcgggct 120
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tcctcttggg 180
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240
ccccatttct gtctttttaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360
gtttgcttt 369

<210> 9
<211> 255
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(255)
<223> 3' terminal sequence. cyclin d1 (prad1:
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9
aaagacagtt tttgggtaat ctttttcttt tgcttaagtc agagatggaa gggggaaaga 60
gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttctgg tatcaaaatg 120
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180
gcggtggcgc cctngcctg gcgccttcag atgtccacgt cccgcacgtc ggtgggtntg 240
caagccaggt ccacc 255

<210> 10
<211> 1325
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1325)
<223> cyclin d1 (prad1: parathyroid adenomatosis
1) (CCND1) gene.

<400> 10

```

gcagtagcag cgagcagcag agtccgcac g ctccggcgag gggcagaaga gcgcgagggga 60
gcgcggggca gcagaagcga gagccgagcg cggaccacgc caggaccac agccctcccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgctgcga agtggaacc 180
atccgccgcg cgtaccccga tgccaacctc ctcaacgacc ggggtgctgcg ggccatgctg 240
aaggcgagg agacctgcgc gccctcgggtg tctacttca aatgtgtgca gaaggaggtc 300
ctgccgtcca tgcggaagat cgtcgccacc tggatgctgg aggtctgcga ggaacagaag 360
tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttcct gtcgctggag 420
cccgtgaaaa agagccgcct gcagctgctg ggggccactt gcatgttcgt ggcctctaag 480
atgaaggaga ccatccccct gacggccgag aagctgtgca tctacaccga cggctccatc 540
cggcccagag agctgctgca aatggagctg ctcttggtga acaagctcaa gtggaacctg 600
gccgcaatga ccccgcacga tttcattgaa cacttcctct ccaaaatgcc agaggcggag 660
gagaacaaac agatcatccg caaacacg cg cagaccttcg ttgcctcttg tgccacagat 720
gtgaagttca tttccaatcc gccctccatg gtggcagcgg ggagcgtggt ggccgcagtg 780
caaggcctga acctgaggag ccccaacaac ttctgtctct actaccgcct cacacgcttc 840
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gccctgctgg agtcaagcct gcgccaggcc cagcagaaca tggaccccaa ggccgcgag 960
gaggaggaag aggaggagga ggaggtggac ctggcttgca caccacacga cgtgcgggac 1020
gtggacatct gaggggcca ggcaggcggg cgccaccgcc accgcagcg agggcggagc 1080
cggccccagg tgctccacat gacagtccct cctctcogga gcattt tgat accagaaggg 1140
aaagcttcat tctccttggt gttggttggt ttttctttg ctctttcccc cttccatctc 1200
tgacttaagc aaaagaaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa                                             1325

```

<210> 11

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. signal transducer and
activator of transcription 1, 91kd (STAT1) gene.

<400> 11

```

atttgaaagt caaagtctta tttgataaag atgtgaatga gagaaatata gtaaaaggat 60
ttaggaagtt caacattttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagtct ggcggtcgaa tttcggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcatcgta ctgaagagct tcactccctt agttttgaaa 240
cccaattgtg ccagcctggg tttggtaatt gacctogaga cgacctctct gcccgttgtg 300
ggtgatctcc aacgtcagcc agctcccagc cggttggggc ctccattcct ttgggtacaa 360
catgctgggt nggcgggaac ccgggg antc tgttccttnt ttcttgact ccaccatgtg 420
ncacggtggg gtttcagntt ttcagaagt                                     449

```

<210> 12

<211> 4003

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4003)

<223> signal transducer and activator of
transcription 1, 91kd (STAT1) gene.

<400> 12

```

attaaacctc tgcgcgagcc cctccgcaga ctctgcgcgc gaaagtttca tttgctgtat 60
gccatcctcg agagctgtct aggttaacgt tgcactctg tgtatataac ctgcacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttggttg aatccccagg cccttggttg 180
ggcacaaggt ggcaggatgt ctacgttgta cgaacttcag cagcttgact caaaattcct 240
ggagcagggt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
acagtgggta gaaaagcaag actgggagca cgctgccaat gatgttt cat ttgccaccat 360
ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttgagaa 420
taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca 480
ggaagaccca atccagatgt ctatgatcat ttacagctgt ctgaaggaag aaaggaaaat 540
tctggaaaac gccagagat ttaat caggc tcagtcgggg aatattcaga gcacagtgtat 600
gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
tatagagcat gaaatcaaga gcttggaaga ttacaagat gaatatgact tcaaatgcaa 720
aaccttgtag aacagagaac acgagaccaa tgggtgtggc aagagtgatc agaaaacaaga 780
acagctgtta ctcaagaaga tgtatttaaat gcttgacaat aagagaaaagg aagtagttca 840
caaaataata gagttgctga atgtcactga acttaccag aatgccctga ttaatgatga 900
actagtggag tggaaagcga gacagcagag cgctgtatt ggggggcgc ccaatgcttg 960
cttgatcag ctgcagaact ggttcactat agttgaggag agtct gcagc aagttcggca 1020
gcagcttaaa aagttggagg aattggaaca gaaatacacc tacgaacatg accctatcac 1080
aaaaaaciaa caagtgttat gggaccgcac cttcagttt ttccagcagc tcattcagag 1140
ctcgtttgtg gtggaagac agccctgcac gccaacgcac cctcagaggc cgctggtctt 1200
gaagacaggg gtccagttca ctgtgaagt gagactgtg gtgaaattgc aagagctgaa 1260
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caccaatggc agtctggcgg ctgaatttcg gcacctgcaa ttgaaagaac agaaaaatg c 1440
tggcaccaga acgaatgagg gtccctctcat cgttactgaa gagcttccact cccttagttt 1500
tgaaacccaa ttgtgccagc ctggtttggg aattgaacct gagacgacct ctctgccctg 1560
tgtggtgatc tccaacgtca gccagctccc gagegggttg gcctccatcc tttggtacaa 1620
catgctggtg gcggaaccca ggaatctgtc ctt ctctctg actccaccat gtgcacgatg 1680
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tgggtgcatc atgggcttca tcagcaagga gcgagagcgt gccctgttga aggaccagca 1980
gccggggacc ttctgtctgc ggttcagtga gagctcccg gaaggggcca tcacattcac 2040
atgggtggag cgggtcccaga acggaggcga acctgacttc catgccc ttg aacctacac 2100
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tgctgagaat attcctgaga atccctgtaa gttactgtat ccaaatttg acaaagacca 2220
tgcttttgga aagtattact ccaggccaaa ggaagcaca gagccaatgg aacttgatgg 2280
ccctaaagga actggatata t caagactga gttgatttct gtgtctgaag ttcaccttc 2340
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gttgatagca agtgaatttt tctctaaact agaaacatca gttactctga agggcatcat 2640
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aacatccaga tacacccaaa gtatcaggac gagaa tgagg gtcccttggg aaaggagaag 2760
ttaagcaaca tctagcaaat gttatgcata aagtcagtgc ccaactgtta taggttggtg 2820
gataaatcag tggttattta gggaactgct tgacgtagga acggtaaat tctgtggag 2880
aattcttaca tgttttcttt gctttaagt taactggcag ttttccattg gtttacctgt 2940
gaaatagtct aaagccaagt ttatatacaa ttatatcagt cctctttcaa aggtagccat 3000
catggatctg taggggggaa aatgtgtatt ttattacatc ttccacattg gctattttaa 3060
gacaaagaca aattctgttt cttgagaaga gaattatgac ttactgttt gttatggctt 3120
aatgacacta gctaatatca atagaaggat gtacatttcc aaattcaca a gttgtgtttg 3180
atatccaaag ctgaatacat tctgttttca tcttggtcac atacaattat ttttacagtt 3240
ctcccaaggg agttaggcta ttcacaacca ctcatcaca agttgaaatt aaccatagat 3300
gtagataaac tcagaaattt aattcatgtt tottaaatgg gctactttgt cctttttgtt 3360
attagggtgg tatttagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420

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ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
tcctatgtaa ctgcattgag aactgcatat gtttgcgtga tatatgtgtt tttcacattt 3540
gcgaatgggt ccattctctc tcctgtactt tttccagaca ctttttttgag tggatgatgt 36 00
ttcgtgaagt atactgtatt tttacotttt tccttcctta tcaactgacac aaaaagtaga 3660
ttaagagatg ggtttgacaa ggttcttccc ttttacatac tgctgtctat gtggctgtat 3720
cttgtttttc cactactgct accacaacta tattatcatg caaatgctgt attcttcttt 3780
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attaaatata atatcgacac agtgctttcc gtggcactgc atacaatctg aggcctcctc 3900
tctcagtttt tatatagatg gcgagaacct aagtttcagt tgattttaca attgaaatga 3960
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```

<210> 13

<211> 167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(167)

<223> 3' terminal sequence. fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 13

```

ccacctctgc tcggtgaaaa ttaagaaatt atgtgtaaga acagcattta gcaaatagct 60
attaaaaaaa gagagaccaa ttttctag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaat ntataatata ttattttatac ntaattt 167

```

<210> 14

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgaggggac 60
tggtggcatg cagtgcctcc cagagaccaa cgttcaagca gttggtagaa gacttggatc 120
gaattctcac tctcacaacc aatgaggaat acttggacct cagccaacct ctcgaacagt 180
attcacctag ttaccctgac ac aagaagtt cttgttcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaaccatgcc ttctcagta tccacacata aacgggcagt 300
gttttaaaac atgaatgact gtgtctggcc tgnccccaa acagggacag gcactggggg 360
aacctaggct acattnaggc aggggaggac ccttgccttc ccaggngttt gttt 414

```

<210> 15
 <211> 4667
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(4667)
 <223> fibroblast growth factor receptor 2
 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 15
 gagcggggcga gggagcgcgc gcggccgccaa caaagctcgg gcgccgcggg gctgcatgcg 60
 gcgtacctgg cccggcgcgg cgactgctct c cgggctggc gggggccggc cgcgagcccc 120
 gggggccccc agggcgcgagc ttgcctgcgc gctctgagcc ttgcgaaactc gcgagcaaag 180
 tttggtggag gcaacgccaa gcctgagtc tttcttctc tcgttcccc aatccgaggg 240
 cagcccgcgg gcgtcatgcc cgcgctctc cgcagcctgg ggtacgcgct gaagcccggg 300
 aggccttggcg ccggcgaaga cccaaggacc actcttctgc gtttgagatt gctccccaca 360
 accccgggct cgtcgctttc tccatccga cccagccggg gcgcggggac aacacaggtc 420
 gcggaggagc gttgccattc aagtgcctgc agcagcagcg gcagcgctc ggttcctgag 480
 cccaccgcag gctgaaggca ttgcgcgtag tccatgccc tagaggaagt g tgcagatgg 540
 gattaacgtc cacatggaga tatggaagag gaccggggat tggtagcgta accatggtca 600
 gctggggctc tttcatctgc ctggctgtgg tcacatggc aaccttgtcc ctggcccggc 660
 cctccttcag tttagttgag gataccacat tagagccaga agagccacca accaaatacc 720
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 atgtcacaga tgccatctca tccggagatg atgaggatga caccgatggg gcggaagatt 1020
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 ggaacccaat gccaaccatg cgggtggctga aaaacgggaa ggagttt aag caggagcatc 1200
 gcattggagg ctacaaggta cgaaaccagc actggagcct cattatggaa agtgtggtcc 1260
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 gtattcatcg agatttagca gcc agaaatg ttttggtaac agaaaacaat gtgatgaaaa 2520

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tagcagactt tggactcgcc agagatatca acaatataga ctattacaaa aagaccacca 2580
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caaaattgga gaaagtattt aataaaacct gttaattttt atactgacaa taaaaatgtt 4620
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```

<210> 16

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)
gene.

<400> 16

```

gtgttgagct cccaaaaggc ttaaaacttg ctttgtgaat gaatgatctt aaatcactag 60
tgaagatgat catggggcat ttgcacatta aagaactaaa atgaaatgaa aaagccatga 120
ctcctcactt aatgctatta aaaaaaaatc tgatttggta aattaacccc acttctcata 180
gtttaatttg gtaatcaacg ttcttgggaa ttc aggttct catggggcacc ctaatagtgt 240
ttagggccgg gggctctgag gctgctgggg gtgatcccga ggaacaagaa gctgccctat 300
taaaagtaat ctacttgagt ttttcccgag tctttgggag ttgttcccta ctgtggggct 360
acttataggg gtaggggccc ccaaatccct cacacttagg tcggccctgc tggcttgcgt 420
tggggctctg aaangcagcc gctaggangt ccccaagcct naacttacc attttctggc 480

```

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ctg

483

<210> 17
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(400)
<223> 3' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 17
ntttatatat attgaacata aattaaaaga atttataaaa cagccacctt tttacagaat 60
aaatgcagac tgaattataa atgcacctcc acgttgaagt tgttttgagt tgcttttcat 120
tttccaataa taaataaata gaatttggtc ttgagtttta gatccacctg agccacggca 180
ggactctaag tcatgaatgg gctttcttcc cttgggtcgt cctgtgcgca gatgntgagt 240
gtgctgaggt tacagatttc attggcccac cagcgtgtat gc tacccttt cgggggtggg 300
cattcgctca ttaattcggg ccagncct cgcgctttct ttcaaaactc cgggatcttg 360
tgcntggagg cgaggnaccc ctctgatggg cttcccgggg 400

<210> 18
<211> 490
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(490)
<223> 5' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 18
cttggagcac tataccaca aactgtccg aggggtgctct tatttctaca gttaccctgc 60
agtttgtgaa tttttgcaga acaataattt actatcaatt atcagagccc atgaagccca 120
agatgctggg tatcgaatgt acaggaagag ccaagccaca ggttttccat cacttattac 180
aattttctct gcccccaatt acctagatgt ctataacaat aaagctgctg tgttgaaata 240
tgaaaacaat gtcatgaata tcaggcagtt taactgttct ccacaccct actgggcttc 300
caaactttat gggatgtttt cacatgggtc ttgacctttt gttgggggga ccccgacac 360
agaggatggc tgggtaaatg tggntcaaca ttatgntct ggatggacgg aactgatttt 420
ctggatggat ggaagcngga tgggaaggca cttacngttt cgtaaggng g ttcttcggg 480
gnttaggttc 490

<210> 19
<211> 2134
<212> DNA/RNA
<213> Artificial Sequence

<220>

13/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),
catalytic subunit, gamma isoform (calcineurin a
gamma) (PPP3CC) gene.

<400> 19

```

gggccaccct tagcagcgggt cgcggtcgggt gccgaagcgg tgttccccgc cttagccgct 60
gcgcctccca agagagcggc cgggtgggccc tcgtcctgtc agtggcgtcg gaggc cggcc 120
tgcggtggcc gcgcccttct ggtgctcgga caccgctgag gagccggggc cgggcacggc 180
tggctgacgg ctccgggcag ctaaggctgc ccgaggagaa ggccggcgcc gcggcgtagg 240
cgcacgtccg gcgggctcct ggagcctgga ggaggccgag ggaccatgt ccgggaggcg 300
cttccacctc tccaccaccg accgcgtcat caa agctgtc ccctttcctc caacccaacg 360
gcttactttc aaggaagtat ttgagaatgg gaaacctaaa gttgatgttt taaaaaacca 420
tttggtaaag gaaggacgac tggaagagga agtagcctta aagataatca atgatggggc 480
tgccatcctg aggcaagaga agactatgat agaagtagat gctccaatca cagtatgtgg 540
tgatattcat ggacaattct ttgacctaat gaagttatgtt gaagttggag gatcacctag 600
taacacacgc tacctctttc tgggtgacta tgtggacaga ggctatttca gtatagagt 660
tgtgtgtgat ttatggagtt taaagattaa tcatcccaaa acattgtttc tgcttcgggg 720
aaatcatgaa tgcaggcatc ttacagacta tttcaccttc aaacaggaat gtc gaatcaa 780
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cctcttaaac cagcagtttc tctgtgtaca tggaggaatg tcacctgaaa ttacttcttt 900
agatgacatt aggaaattag acaggtttac ggaacctccc gcctttggac ctgtgtgtga 960
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gaaaatgaaa agcaactcaa aacaacttca acctggaggt gcatttataa ttcagtctgc 1920
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aaaaagtgca tctgttttgt ttttcccttt tttctccata attttaagaa atgaatctga 2040
ttgttgtcaa cacatttgtg aagtcttgtg cta taaaggg gaacttcccc taataaaagg 2100
gccttgga aa cctcaaacct gggtttctga cccc 2134

```

<210> 20

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)
gene.

<400> 20

```
atccatTTtat tatatccaat gctaaacact accacttgga ctctaagata tgTTTtatgcc 60
tctctgtTTta ttctagtTTt ttaaaaatca aatatacaag atctacaatt atTTtatatcc 120
aagatgtcta caccactgcc taagaagcta ttaaaatat t tgtatttTtg caatgggnacc 180
cattattcac atgggcctag gattaaaaag tcaatttata ttngnaataa attTntccaa 240
aaaaacca                                     248
```

<210> 21

<211> 427

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(427)

<223> 5' terminal sequence. ests (EST T90726)
gene.

<400> 21

```
taagatacga acgagaaacc tgatttattg ctcatccttc ccttgccctcc ctaatggcaa 60
gcaaaaactct gaacatctga aaaggatgta gttctggaca aatcct gact acccagagga 120
aactcactgt gagattgctg ttgatttgaa gggTgcttTc actaaggTta tattTTtaaag 180
tagaataaca catgctgagt gtaaaactggg cTTTggattg gTcagctgca gtagtacaaa 240
aacagcatag aatttgagga aaactaaaac Tgctatgaga taggctatga ggaaaactta 300
aaactggcta Tgtggtagga aatg atgTta aanttatgtg gggaaagTTt ttcccctccn 360
tattacttca cattacaggc cTTTngaggg gcntctgggc tctgnaccn gTTTgatggg 420
cctttga                                     427
```

<210> 22

<211> 294

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(294)

<223> 3' terminal sequence. sry (sex determining
region y)-box 4 (SOX4) gene.

<400> 22

```
tttcttgTTt ttctTTTTt ttttccgaaa ccactcgccc tccactgact gcccctgtac 60
cacatcaaac agTctcctct cctccacgcc tccggggTct gggaagtctc acctcactga 120
tttcacgtag aaaagaaggc ggaggccagc agccgcgcgc ncaagctccc caacgtgcaa 180
atccatttca gTTtgaccgt gaacccctt ccagTtctgTg tctcctccg cccccgcccc 240
tagctcccgTg Tgctggnttc caacggggTt ntcgggtcat ttccTagcgc cggt 294
```

<210> 23

<211> 362

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(362)

<223> 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

<400> 23

```

ttccggactt gtctgcaccc ccagcaagaa ggcgagttag ttttctagag acttgaagga 60
gtctccccct tcctgcatca ccaccttgggt tttgttttat ttgtcttctt ggtcaagaaa 120
ggaggggaga acccagcgca cccctcccc ctttttttaa acgcgtgatg aagacagaag 180
gctccggggt gacgaatttg gccgatggag nat gtttttg gggaacgccg ggactgagag 240
actccacggc agggcggaatt cccgtttggg gctttttttt tcttccctct ttttccccct 300
gccccttttg canccgngg agggagntgt tnaaggggag ggagggccag ccagtgttga 360
cc

```

<210> 24

<211> 2797

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2797)

<223> sry (sex determining region y) -box 4 (SOX4) gene.

<400> 24

```

ttccccagca ttcgagaaac tcctctctac tttagcacgg tctccagact cagccgagag 60
acagcaaact gcagcgcggt gagagagcga gagagaggga gagagagact ctccagcctg 120
ggaactataa ctctcttgcg agaggcggag aactccttcc ccaaattctt tggggacttt 180
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ccggcctcga gctgggaate gcctcctccc ccacgcccgg ctccaccgcc t ccacgggcg 480
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tgcacaacgc cgagatctcc aagcggctgg gcaaacgctg gaagctgctc aaagacagcg 660
acaagatccc tttcattcga gaggcggagc ggctgcgcct caagcacatg gctgactacc 720
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tgcgcgccgc ctgcgccgc ccgtccagcg cgcctcgcga cgcgtcctc tcggcctcgt 1500
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```

```

cgctcgtcggc gctcgaccgg gacctggatt ttaacttcga gcccggtcc ggctcgact 1680
tcgagttccc ggactactgc acgcccagg tgagcgagat gatctcggga gactggctcg 1740
agtccagcat ctccaacctg gttttcacct actgaa gggc gcgcaggcag ggagaagggc 1800
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```

<210> 25

<211> 352

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(352)

<223> 5' terminal sequence. ring finger protein 5
(RNF5) gene.

<400> 25

```

acggggggccc caacnanant cgcgagcngg gcgtggcggg gcgcaccttc gaatgt anta 60
tatgtttgga gactgctcgg gaagctgttg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacacggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cagagagaag gttgtcccg tttatggcg agggagccag aagcccagg 240
atcccagatt aaaaactcca cccgcggcgg aggcc agaga ccagctccg agagcagagg 300
gggattccag ccatttgggtg ataccggggg cttccacttn ttcatttgggt gt 352

```

<210> 26

<211> 543

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(543)

<223> ring finger protein 5 (RNF5) gene.

<400> 26

```

atggcagcag cggaggagga ggacgggggg cccgaagggc caaatcgca gcggggcggg 60
gcgggcgcga ccttcgaatg taatatatgt ttggagactg ctcggaagc tgtggtcagt 120

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gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
cggcaagagt gtccagtatg taaagctggg atcagcagag agaaggttgt cccgctttat 240
gggcgagggg gccagaagcc ccaggatccc agattaaaaa ctccaccccg ccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
cactttcat ttggtgttgg tgcttttccc ttt ggctttt tcaccaccgt cttcaatgcc 420
catgagcctt tccgccgggg tacagggtgtg gatctgggac agggtcaccc agcctccagc 480
tggcaggatt ccctcttcc ttttctcgcc atcttcttct ttttttggct gctcagtatt 540
tga 543

```

<210> 27
 <211> 397
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(397)
 <223> 3' terminal sequence. axl receptor tyrosine
 kinase (AXL) gene.

```

<400> 27
gccgtggggt gggaaagtgg gaag gtggag ttttcccag tggcagtgt tagcttggat 60
cctgagaggg agtaccaggt ggagggttgt ctccagcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gcntccagca ggatggacct cagccgcagt naggcagcta caggaatcct tagggtctgg 240
ctgggttggg gggtcagctc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatnttn acatagagga tttcgtcagg ctctgggggc aggangcaan gcctttcagt 360
ntgttctcca aatcttccn caactctnta aaacttt 397

```

<210> 28
 <211> 418
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(418)
 <223> 5' terminal sequence. axl receptor tyrosine
 kinase (AXL) gene.

```

<400> 28
ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
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agtctagctg accgtgtcta caccagcaag agcgatgtgt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaaccoca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccagggaa atcgccgtgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcggcg tncctgggga gcttaaattc cccaggggnc ccgnccaatt 360
ttttacaaag cttncgggga agattttttg gagnacacac ttttaagggc tttncctt 418

```

<210> 29
 <211> 5015
 <212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

```

gagtggagtt ctggaggaat gtttaccaga cacagagccc agagggacag cgcccagagc 60
ccagatagag agacacggcc tcactggctc agcaccaggg tccccctccc cctcctcagc 120
tccctcctctg gcccctttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccaggtg gcccctggct ctggcctggt gggcggaggc aaagggggag ccaggggcgg 240
agaaagggtt gcccaagtct gggagtgagg gaaggaggca ggggtgctga gaaggcggct 300
gctgggcaga gccggtggca agggcctc cc ctgccgtgt gccaggcagg cagtgccaaa 360
tccggggagc ctggagctgg ggggaggggc ggggacagcc cggcccgtg ccccctcccc 420
cgctgggagc ccagcaactt ctgaggaaag tttggcacc atggcgtggc ggtgccccag 480
gatgggcagg gtcccgtctg cctggtgctt ggcgctgtgc ggctgggcgt gcatggcccc 540
caggggcacg caggctgaag aaagtccctt cgtgggcaac ccagggaata tcacaggtgc 600
ccggggactc acgggcaccc ttcggtgtca gctccagggt cagggagagc ccccagaggt 660
acattggctt cgggatggac agatcctgga gctcgcggac agcaccacaga cccaggtgcc 720
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gacgatgaag attgccatct gcacgaggtc agagctggag gatttctctga gtgaagcgg 2220
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ggatgcctcc tttccgcagg ggatggacga tctcccacct ttcgggccat gttgcccccg 4920
tgagccaatc cctcaccttc tgagtacaga gtgtggactc tgggtgcctcc agaggggctc 4980
aggtcacata aaactttgta tatcaacgaa aaaaa 5015

```

<210> 30

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB)
gene.

<400> 30

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aacacgtcac cggagagatg atgggtggcc atgcatccgc atcctgggct ggggagtgga 60
gaatggcaca ccctactggc tgg ttgcaa ctcttggaac actgactggg gtgacaatgg 120
cttcttttaa atactcagag gacaggatca ctgtggaatc gaatcagaag tgggtggctg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggct tgtcgtgcca 240
gtcctggggg gcgagatcgg ggtagaaatg cattttattc tttaagttca cgttaaggat 300
acaagttttc agacagggtc tgaaagggan tgggatttng gccaaacatc agacctgttc 360
tttcccaagg gaggaccaag ttctgtgggt aacattcccc agcctnttgg tttaacagtt 420
gncaggacag ggcctgtt 439

```

20/292

<210> 31
 <211> 1996
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1996)
 <223> cathepsin b (CTSB) gene.

<400> 31
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 ctgggctggg gtgcagtggg ggcaccacg g ctacggcag cctcagccac ccagatgtaa 120
 gcgatctggg tcccacctca gccctccgag tagtggatct aggatccggc ttccaacatg 180
 tggcagctct gggcctccct ctgctgcctg ctgggtgttg ccaatgcccg gagcaggccc 240
 tctttccatc ccctgtcgga tgagctgggt aactatgtca acaaacggaa taccacgtgg 300
 caggccgggc acaacttcta caacgtggac atgagctact tgaagaggct atgtggtacc 360
 ttcttgggtg ggcccaagcc accccagaga gttatgttta ccgaggacct gaagctgcct 420
 gcaagcttcg atgcacggga acaatggcca cagtgtccca ccatcaaaga gatcagagac 480
 cagggtcctt gtggctcctg ctgggccttc ggggctgtgg aagccatct c tgaccggatc 540
 tgcattccaca ccaatgcgca cgtcagcgtg gaggtgtcgg cggaggacct gctcacatgc 600
 tgtggcagca tgtgtgggga cggctgtaat ggtggctatc ctgctgaagc ttggaacttc 660
 tggacaagaa aaggcctggg ttctgtgtgg ctctatgaat cccatgtagg gtgcagaccg 720
 tactccatcc ctccctgtga gcaccac gtc aacggctccc ggcccccatg cacgggggag 780
 ggagataccc ccaagtgtag caagatctgt gagcctggct acagcccgac ctacaaacag 840
 gacaagcact acggatacaa ttctacagc gtctccaata gcgagaagga catcatggcc 900
 gagatctaca aaaacggccc cgtggaggga gctttctctg tgtattcgga ctctctgctc 960
 tacaagtcag gagtgtacca acacgtcacc ggagagatga tgggtggcca tgccatccgc 1020
 atcctgggct ggggagtggg gaatggcaca ccctactggc tgggtgcca ctctggaac 1080
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 gccgtgggcc tgtcgtgcca gtcttggggg cgagatcggg gtagaaatgc atttttattc 1260
 ttaagttcac gtaagataca agtttcaggc aggtcttgaa ggactggatt ggccaaacat 1320
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 gacaggccat gtgagccac c gctgccagca cagagcgtcc ttccccctgt agactagtgc 1440
 cgtgggagta cctgctgccc agctgctgtg gccccctccg tgatccatcc atctccagg 1500
 agcaagacag agacgcagga tggaaagcgg agttcctaac aggatgaaag ttcccccatc 1560
 agttccccca gtacctccaa gcaagtagct ttccacatth gtcacagaaa tcagagga ga 1620
 gatggtgttg ggagcccttt ggagaacgcc agtctccagg tccccctgca tctatcgagt 1680
 ttgcaatgtc acaacctctc tgatcttggt ctacagcatg ttctttaata gaagttttat 1740
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 tttgcagatt gcctccta at gacgcggctc aa aaggaaac caagtgggtc ggagttgttt 1860
 ctgaccact gatctctact accacaagga aaatagttta ggagaaacca gcttttactg 1920
 tttttgaaaa attacagctt caccctgtca agttaacaag gaatgcctgt gcccaataaaa 1980
 ggtttctcca acttga 1996

<210> 32
 <211> 492
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32
ttccattttt cttctttttat tagaattttt tcattttttt tctcaaaatt tttatctaaa 60
aacaaacaga aaaaagaagg aaaaaaagaa aaaaaaatta ttggaaactt catggttcaa 120
gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaag caccctcttg ggggacagca gagccagg ga cagccccccc ccacgcccag 240
cctccgtctg agggaagatg ggcagagtca cagtgggtgc gaggggcccag aagggttggg 300
aggngggcag gggcgggcgg ggtcacagga agtagttcgg ccacggcttt ctttgggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttaccaagat tggcttncca cattttcca cagcgggtaca 480
agttagtttt tg 492

<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33
ctnttcatgg gggactttgt ggaccgtggc ttctatagcg tcgaaacgtt nctnctgctg 60
ctggcactta aggttcgcta tcttgatcgc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggtcta tggcttctac gatgagtgcg tgcgcaagta acggctcggg 180
gactgtgtgg cgctactgca ctgagatctt tgactacctc agcctgtcag ccatcatcga 240
tngaaagaat cttctgcgtg cacggggggc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt 330

<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),
catalytic subunit (PPP4C) gene.

<400> 34
gccacgaagg cgggagagcc ggaaccggag tcgcagcggc ggagaccct gtgcggtgcg 60
gagggggcgg cgccccgac tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
aggccctgtg cgctaaggcc agagagatct tggtagagga gagcaacgtg cagaggggtg 240
actcgccagt cacagtgtgc ggcgacatcc atggacaatt ctatgacctc aaagagctgt 300
tcagagtagg tggcgacgtc cctgagacca actacctctt catgggggac tttgtggacc 360
gtggcttcta tagcgtcgaa acgttcctcc tgctgctggc acttaaggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtgcga gatcacgcag gtctatggct 480

22/292

```
tctacgatga gtgcctgcgc aagtacggct cgggtgactgt gtggcgctac tgcactgaga 540
tcttttgacta cctcagcctg tcagccatca tcgatggcaa gatcttctgc gtgcacgggg 600
gcctctcccc ctccatccag accctgg atc agattcggac aatcgaccga aagcaagagg 660
tgcctcatga tgggcccattg tgtgacctcc tctgggtctga ccagaagac accacagggt 720
ggggcgtag ccccgaggga gccggctacc tatttggcag tgacgtggtg gccagttca 780
acgcagccaa tgacattgac atgatctgcc gtgcccacca actggtgatg gaaggttaca 840
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gtgggaatgt ggcagccatc ttggagctgg acgagcatct ccagaaagat ttcattcatct 960
ttgaggctgc tccccaaagag acacggggca tcccctccaa gaagcccgtg gccgactact 1020
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ctctgccatc ttcctcagac ggaggctggg cgtggggggg gctgtcctgg ctctgctgtc 1140
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tgttctctct cctctctccc cacttgaacc atgaagtttc caataatfff tttttctfff 1260
tttcttctt ttttctgttt gtttttagat aaaaattttg agaaaaaaaa tgaaaaaatt 1320
ctaataaaag aagaaaaatg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1429
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<210> 35
<211> 493
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(493)
<223> 3' terminal sequence. ests (EST T79867)
gene.

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<400> 35
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tcccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac ccactctttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacia tataatatct 180
aacttcagta aatcaaagac aatfffgaaa gaagccaaag ggaaaaaaat gacctgaaga 240
gtcctgttta anttttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttctctac ccaggaccen ttcccacctc actagggnac tttggantgg gatatatgtg 360
gggaaactct tgggcttttc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc cttgggncac tcccngttg gatgggtntt gggggaggag noctgntggg 480
gntttttccc at 493
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<210> 36
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(354)
<223> 3' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) g ene.

```
<400> 36
tttttgtttt ttatttcaaa aaaataatff ataaaacgcc atttgctcct gttttcggca 60
ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgctgg gccagcagca 120
```

23/292

```
gcagggggag gtnthggggaa aggggggttca gaggcccaga acctcctgct ggtattggga 180
ggcaggaggt ttagcatagc agctctcca g ccaggctcag ccaaaccgg gatggggact 240
aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300
cacggcagct cccaagggca aggggcacgg ccttngggac angggcacag caac 354
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<210> 37

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 5' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) gene.

<400> 37

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ggcagcagcg ccctcccaga ggccctacctt caagcagctg gtggaggcgc tggacaaggt 120
ctgctggccg tctctgagga gtacctcgac ctccgcctga ccttcggacc ctattcccc 180
tctgggtggg aacgccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240
ccctgccatt ggggattcag ctccctccct ttgggtctng ggggtgcagac atga gcaagg 300
ctnaagggtt ttgcaaggga catagggttg gtgggc 336
```

<210> 38

<211> 3015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3015)

<223> fibroblast growth factor receptor 4 (FGFR4)
gene.

<400> 38

```
ccgaggagcg ctcggtgtgt ctgoggaccc tgccgcgtgc aggggtcgcg gccggctgga 60
gctgggagtg aggcggcgga ggagccaggt gaggaggagc caggaaggca gttggtggga 120
agtccagctt gggtccttga gagctgtgag aaggagatgc ggctgctgct gg ccctgttg 180
ggggtcctgc tgagtgtgcc tgggcctcca gtcttgtccc tggaggcctc tgaggaagt 240
gagcttgagc cctgcctggc tcccagcctg gagcagcaag agcaggagct gacagtagcc 300
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gagggcagtc gcctggcacc tgctggcgt gtacggggct ggaggggccc cctagagatt 420
gccagcttcc tacctgagga tgctggcgc tacctctgcc tggcacgagg ctccatgatc 480
gtcctgcaga atctcacctt gattacaggt gactccttga cctccagcaa cgatgatgag 540
gacccaagt cccataggga cctctogaat aggcacagtt acccccagca agcaccctac 600
tgacacacc ccagcgcgat ggagaagaaa ctgcatgcag tacctgcggg gaacaccgtc 660
aagttccgct gtccagctgc aggcacccc acgcccacca tccgctggct taaggatgga 720
caggcctttc atggggagaa ccgcattgga ggcattcggc tgcgccatca gcactggagt 780
ctcgtgatgg agagcgtggg gccctcggac cgcggcacat acacctgcct ggtagagaac 840
gctgtgggca gcatccgcta taactacctg ctatagtggtc tggagcggc cccgcaccgg 900
cccatcctgc aggcgggct cccggccaac accacagccg tgggtggcag cgacgtggag 960
ctgctgtgca aggtgtacag cgatgccag cccacatcc agtggctgaa gcacatcgctc 1020
```

24/292

```

atcaacggca gcagcttcgg agccgacg gt ttcccctatg tgcaagtcct aaagactgca 1080
gacatcaata gctcagaggt ggaggtcctg tacctgcgga acgtgtcagc cgaggacgca 1140
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acggtgctgc cagaggagga cccacatgg accgcagcag cgcccagggc caggtatacg 1260
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tttttttgaa ataaa
3015

```

<210> 39

<211> 252

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(252)

<223> 3' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 39

```

gtgtgattta ttatgtttta gattggttta taaggcttaa atatatctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtgtt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata tticctcaat gcaaatntca aatctgcagc 180
accatttaga agcttccact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta
252

```

<210> 40

<211> 382

25/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(382)

<223> 5' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 40

```
ctnacnttca aacgganntg gaa ttatttc caaagggtat tggatgaagaa atatgcttcg 60
gaaagaaatg gagttaacgt gataagtggg ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gattttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcctc cttcatcctg cctcacggc ctgacaacga ggagagctgc 300
aatagctcag aggacgnatt caaaatgggt agnagggaact catgaaggnt gcacacagct 360
agggtncgtt gacctttgna cc 382
```

<210> 41

<211> 2592

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2592)

<223> ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 41

```
atggcaagga ggagctcggt ccagtcgtgt ca gataatat cctgttcac ttttgccgtt 60
ggagtcaata tctgcttagg attcactgca catcgaatta agagagcaga aggatgggag 120
gaaggtcctc ctacagtgc atcagactcc cctggacca acatctccg atcttgcaag 180
ggcaggtgct ttgaacttca agaggctgga cctcctgatt gtgctgtgga caacttgtgt 240
aagagctata ccagttgctg ccatgacttt gatgagctgt gtttgaagac agcccgtgcg 300
tgaggagtgt ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttggccag gggagactgc tgtaccaatt accaagtggg ttgcaaagga 420
gagtcgcatt gggttgatga tgaactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcatc atacatgaag 540
aaaggcagca aagtcatgcc taatattgaa aaactaaggc cttgtggcac aactctccc 600
tacctaggcg cgggtgtacc aactaaaacc ttctctaact tatacacttt ggccactggg 660
ctatatccag aatcacatgg aattgttggc a attcaatgt atgactcctgt atttgatgcc 720
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tggttacag ccaccaagca aggggtgaaa gctggaacat tcttttggtc tgtgtcatc 840
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gctaaatatg accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
tttaagcctt acttgaaaca gcaccttccc aaacgtttgc actatgcca caacagaaga 1320
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tatgactatg atggcttaca tgacacagaa gacaaaataa aacagtacgt ggaaggcagt 2280
tccattcctg ttccaactca ctactacagc atcatcaoca gctgtctgga ttctactcag 2340
cctgccgaca agtgtgacgg ccctctctct gtgtctctct tcactcctgcc tcaccggcct 2400
gacaacgagg agagctgcaa tagctc agag gacgaatcaa aatgggtaga agaactcatg 2460
aagatgcaca cagctagggt gcgtgacatt gaacatctca ccagcctgga cttcttccga 2520
aagaccagcc gcagctaccc agaaatcctg aactcaaga catacctgca tacatatgag 2580
agcgagattt aa 2592

```

<210> 42

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

```

<223> 3' terminal sequence. v-rel avian
      reticuloendotheliosis viral oncogene homolog a
      (nuclear factor of kappa light polypeptide gene
      enhancer in b-cells 3 (p65)) (RELA) gene.

```

<400> 42

```

acagatttat tagttcagag tagaaagagc aagagtocaa gtgctttgat tgttcagtaa 60
aaactatgcc tccngactgg agagctgcca gctgtctctc cccactctt aacaacttac 120
cctactatta aggcacttga gaagagggag agcaagggaag tcccagacca aacccttct 180
ggatccnggg ngagagccag tgctgttgcg ttggtnttct tcagccatgg ttgagcaagg 240
aaagagccgg cagagacctc tgtagggcag gaaggccagc ccctcaaacg ctgggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctgggtat ctggggggcgt tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gctttntggg gctcaaagg 420
ctttacctcc agcctgcttc tntctctagg gngagtaccc agaagct 467

```

<210> 43

<211> 2444

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog a (nuclear factor of kappa light
polypeptide gene enhancer in b -cells 3 (p65))
(RELA) gene.

<400> 43

```
ggcacgaggc ggggccgggt cgcagctggg cccgcggcat ggacgaactg ttccccctca 60
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gctccgcggg cagcatccca ggcgagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctccctgggtc a ccaaggacc 240
ctcctcaccg gcctcaccac cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
aggctgagct ctgcccgga cgcctgcatt acagtttcca gaacctggga atccagtgtg 360
tgaagaagcg ggacctggag caggctatca gtcagcgcac ccagaccaac aacaaccct 420
tccaagttcc tatagaagag cagcgtgggg actacgacct gaatgctgtg cggctctgct 480
tccagtgtag agtgcgggac ccacagggca ggccccccg cctgccgcct gtcctttctc 540
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gaaactcttg cagctgcctc ggtggggatg agatcttct actgtgtgac aaggtgcaga 660
aagaggacat tgaggtgtat ttacggggac caggctggga ggccccgaggc tccttttctc 720
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caggaggcat agtttttagt gaacaatcaa agcacttgga ctcttgctct ttctactctg 2400
aactaataaa gctgttgcca agctggacgg cagcagctcg tgcc 2444
```

<210> 44

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell
kinase (ITK) gene.

<400> 44

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ggatcatgaa caactttatc ctcttgaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaactt taaagtccgc ttctttgtgt taaccaaaagc cagcctgg ca 180
tactttgaag atcgatcatg gaagaagcgc acgctgaagg ggtccattga gctctccga 240
attcaaatgt gttgaggttg tgaaaagtga catcagcatc ccatgccact attaaatacc 300
cgttttcagg tnggtgcatg acaacttacc tcctnttatg gtgtttgntt ccagntcgtg 360
aggaggccgg ncagcgttng g                                     381
```

<210> 45

<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

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attcagatat gtttgaaaca ttcttaaggc tacaaaacag aacatagaaa aataaacagg 120
aatatatcca acacttacaa aaagtgtatg gataaagaat ataaagtact agtttccttt 180
taacacttca aaagatatgt atatatactt ttttttacaa gtaacatcac aaatgctcac 240
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acataaaaatt ttctagctct gtaacacaat gcaattttta atccattcag taagttcaac 360
cccaaagtgg ccgcttccca gcattaagac atgcacccac cctctttcta agatttttcta 420
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```

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<210> 48

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 3' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 48

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tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaaggg gttcctgagc 180
aggtagcctg gggggacacc agaggngcct ctggggctcc tcctgctctg atgccaccaa 240
gtgctcaaaa agagcttctg cagtgggggtt gggattgctt ttttgacctt taaaatatta 300
tatgtttaag gttagggggg atgaaggggg gaatgccctt tttatttttc ttcccatttt 360
aaaaatatgt gttttctagg catccaaata tagggggctg tggcctggga gggctaggcc 420
ccctttgccg ggttcact 438

```

<210> 49

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating
factor 1 (macrophage) (CSF1) gene.

<400> 49

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ctggggctga gcaggttatc cctgtcagga gccctgggac tgggctgcat ctacagcccca 180
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caacagtgat ggaccttcca actcttcacc caccctct accattcacc tctaaaccag 300
gggaagccag gggtngggag agcant cagg gagagccagg gcttcagttt tccaattgct 360
ggggangggc ttccattttt tggggccagc 390
```

<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage)
(CSF1) gene.

<400> 50

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ccgtatgacc gcgcccggcg cgcgccggcg ctgccctccc acgacatggc tgggctccct 180
gctgttggtg gtctgtctcc tggcgagcag gagtatcacc gaggaggtgt cggagtactg 240
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```

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ccctcacca tcctggacac tctcgtttgt caatgtccct ctgaaaatgt gacgcccagc 1860
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```

<210> 51

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 51

```

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ccactggtcc ctggttaagt ttgtgctggc catcactctt tgagggatca nccgctcaga 180
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gtagggaccc caagagcacg gcagtctcag ggggggcagt agatctcatc gctaagggat 300
tcctttcctt cacttnggag ggaggaaaag tttctggggg gatgtcctgg ggatgagctt 360
ccttcagcca catctttcag ggnaggact ttnggcc 397

```

<210> 52

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 5' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 52

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gggaagtgtg gtactttggc ctccactatg tggatnaata aaggatttcc tacctgg gct 300
gaagctggat aagaaggtgt ctgcccagga ggtcaggaag gagaatcccc tccagttaa 360

```

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```
gttccggggc caagttctac cctgaagatg tgggctgagg agctcattcc agggacattc 420
accagaaat tttntttcnt ccaagtgaag gaagggattc ttaggcgn 468
```

<210> 53

<211> 3064

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3064)

<223> villin 2 (ezrin) (VIL2) gene.

<400> 53

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<210> 54

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 3' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 54

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ccaaacccta tttaccaaaa ttttcccggt cttttaaggt ttccatttgg aaaccaaatt 360
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<210> 55

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 55

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39/292

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42/292

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<210> 57
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
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 <223> 5' terminal sequence. mucin 1, transmembrane
 (MUC1) gene.

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 <222> (1)..(1721)
 <223> mucin 1, transmembrane (MUC1) gene.

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agaagttcag tgcccagctc tactgagaag aatgctgtga gtatgaccag cagcgtactc 240
tccagccaca gccccggttc aggtctctcc accactca gg gacaggatgt cactctggcc 300
ccggccacgg aaccagcttc aggttcagct gccacctggg gacaggatgt cacctcggtc 360
ccagtcacca ggccagccct gggctccacc accccgccag cccacgatgt cacctcagcc 420
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gtacctctc tcacctctc caatcacaga acttct cccc agttgtctac tggggctctc 960
ttctttttcc tgtcttttca catttcaaac ctccagttta attcctctct ggaagatccc 1020

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agcaccgact actaccaaga gctgcagaga gacatttctg aaatgttttt gcagatttat 1080
aaacaagggg gttttctggg cctctccaat attaagttca ggccaggatc tgtggtggtg 1140
caattgactc tggccttccg agaaggtacc atcaatgtcc acgacgtgga gacacagttc 1200
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tgagctgagt ggccagccag tgccattcca ctccactcag ggctctctgg gccagtcctc 1680
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```

<210> 59

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 3' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 59

```

ttagccaatt gatttttttg gtggttgttt tttttaaaagc caatttctga gcttttgtgg 6 0
ggtgtttcta aaaagccaat tagttttaag agggttgttg tggggggggg ggaagggggg 120
tagtttaatg ttttgatttt ttatgtgtgg ggataatttg ggataatttg gggggagggt 180
atgtgaaggg tgtttaaaagc caatcgattt tgtacatgtt tgaagatgct gctgtgcttc 240
ctcagcccgga tggagggggc cgaggagagt agcctgtttc ggggaggcng ggcacgggga 300
ctgggtcang agaagcccca gggggaccgt ngaccccaga gattttcggg atggaaccc 359

```

<210> 60

<211> 410

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(410)

<223> 5' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 60

```

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ccaatatgac acctgggaag cagtccacc agcgctgca ggggcnctgc ctgccctcct 120
gcgtgcccgc cggggtc acg tgctcgccaa ggagctcgag gcgttcaggg aggccaaacg 180
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gatggggcag caatcggaag tgagcaaaat tgccgcaagt ntttcagccc ggcgncacca 300
ttccttgtag cttntntntt gaaccacgga gtttttcttn aggtttccat tccngaaaa t 360
tttttnggtt ttncaaagtt cccttggggg gttttttttn tttgaaacca 410

```

<210> 61
<211> 1356
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1356)
<223> insulin-like growth factor 2 (somatomedin a)
(IGF2) gene.

<400> 61
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ctctgcccc ctctatcctt gatacaacag ctgacctcat ttcccgatac cttttccccc 300
ccgaaaagta caacatctgg cccgccccag cccgaagaca gcccgctctc cctggacaat 360
cagacgaatt ctcccccccc ccccaaaa aa aaaagccatc cccccgctct gccccgtcgc 420
acattcgcc cccgcgactc ggccagagcg gcgctggcag aggagtgtcc ggcaggaggg 480
ccaacgccc ctgttcggtt tgcgacacgc agcagggagg tggcgggcag cgtcgccggc 540
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gattggcttt aaacaccctt cacataccct ccccc 1356

<210> 62
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(474)
<223> 3' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 62
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gcgtatgata ggcgctggag gggcacgctt agaaccatgc accaacaagg gcaggagaaa 120
acaaaatggt agccaggtgt tcttggtcat gccattgaat ttgggtctgt tctcagaaac 180
tctggaattg aagaagttgc aganaccgaa gataaaatgg tcgtttggag cagaaacacc 240
tgattttctca tcagtgcata caaccacagg aagacggccc ccaacatt ct tccccagagg 300

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gttctggtggc tgggtgggga tccctcattt cccatgttaa gcttgaggaa gagatttcag 360
ggtaggctcc ctgcaggga actacttgct cctcaacttt nggcctccca tagcatattt 420
tnaaagccag naagggtttt ttaaccctt ntttggaag cccgattggc att 474

```

<210> 63

<211> 457

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(457)

<223> 5' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 63

```

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cagctcccag tcccagacct caaggatctt gctgtcctcc atgccatccg cttccaagac 120
gggttaaagt cttttcttgc tttcaaataat gctatggagc cacagttgag gacagtagtt 180
tcctgcagga gcctaccctg aaatctcttc tcag cttaac atgggaaatg aggatcccac 240
cagccccagg aaccctctgg gggaaggaaat gttggggggc cgtcttcctg tgggttgtat 300
tgcantgatg gaggaatca ggtgtttttt gntccaaacg gaccatttta ntctttcgtg 360
gntttgcaan ttttttcaan ttccagagtt ttttgaggna caggacccaa nttcantggg 420
catgnaccag gaacatcggg gttaaccntt tttgttt 457

```

<210> 64

<211> 3149

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3149)

<223> egf-like module containing, mucin-like,
hormone receptor-like sequence 1 (EMR1) gene.

<400> 64

```

ctaaagtttt tttctttgaa tgacagaact acagcataat gcgtggcttc aacctgctcc 60
tcttctgggg atgttgtgtt atgcacagct gggaaggga cataagaccc acacggaaac 120
caaacacaaa gggttaataac tgtagagaca gtaccttggt c ccagcttat gccacctgca 180
ccaatacggg ggacagttac tattgcactt gcaacaagg ctctctgtcc agcaatgggc 240
aaaatcactt caaggatcca ggagtgcgat gcaaagatat tgatgaatgt tctcaaagcc 300
cccagccctg tggctctaac tcactctgca aaaacctgtc agggagggtac aagtgcagct 360
gtttagatgg tttctcttct cccactggaa atgactgggt cccaggaaag ccgggcaatt 420
tctctgttac tgatatcaat gactgcctca ccagcagggt ctgccctgag cattctgact 480
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ccacctgtga agacgtgaat gaatgtgcag atccaagagc ttgccagag catgcaactt 600
gtaataacac tggttgaaac tactcttgtt tctgcaaccc aggatttgaa tccagcagtg 660
gccacttgag ttgccagggt ctcaaagcat cgtgtgaaga tattgatgaa tgcactgaaa 720
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```



```

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ccgataataa gcagatc cag caatgccaaag aggggaaccgc agtgaaacct gcataatgtct 1080
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gttttctcct gcccttgttg gtgcatggtt ctaagcgtgc cctccagcg cctatcatac 3060
gcctgacaca gagaacctct caataaatga tttgtgcct gtctgactga tttaccctaa 3120
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3149

```

<210> 65

<211> 412

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(412)

<223> 3' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 65

```

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tgaaggttta cagactggtc aaggaaggac gaacagagag aatggggtct gaggggtcac 120
atcccgtgga ggggtggcggg gctcctggcc tcgtctgggt gaggttggga gcctcgctgg 180
ggctgcggtc ccagagcttc ggcaaagcca ccaggccttg gggagcaggg ctttggcaag 240
caggccgctt cgga gaaaaa caatgactaa ctcactctga cagggcagtt ggggagactt 300
taggacaggn ttcaacattc agatgggctt ggaccncctt tttccattnc ggccaaggaa 360

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ccccggggcn agggngnaaa gcaattncaa agccttttagg aaatttcaat tt 412

<210> 66

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 5' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 66

```
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ttgagacccc gaggcagctt cccgagggag actgctcaga caggaactgc aggacagaag 180
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catttcttaa gggttgcatt gcttttcccc ttgcgccgcg ttctttggcg catggaagga 360
ggcggttcca gccatcttga tgtttgatcc ngttttcagt nttccccant tgcctnttca 420
gggatngagt tagttcattt tt 442
```

<210> 67

<211> 5737

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5737)

<223> k1aa0427 gene product (K1AA0427) gene.

<400> 67

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```

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tgagcacac actttgatga gcccccccg aaatgatgtc agagcctagc cgcttctt a 3540
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cgaggcagct tcccaggga gactgctcag acaggaactg caggacagaa gtggatgcc 4680
cacagacctt gggccccct ccaagctcat cccctctctg tggcatgagg aaggcccgct 4740
ccgagttgac ctctgaatgt atgtgatgag aggcagagct ggatattgca tttctaaggc 4800

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ttgcattgct ttccccctgc ccgcgggttct tggcg catgg aagaggcggt ccagccatct 4860
gatgttgatc ctgtctcagt ctccccactg cctgtcagga tgagttagtc attgtttttc 4920
tccgaggcgg cctgtcttgc acagccctgc tccccaaaggc ctggtggctt tgccgaagct 4980
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```

<210> 68

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 68

```

tctttctttc tttccttaac tggctacatg cttagaaact gcactgggtca aacttgattt 60
tctttttaaa gcctcaaaac atttttattg tcaggaaagc ttttcagtgg ccagggatca 120
gtctcatggc cgtagaagca gccaaattcc tctgcctttg ccttcccttc aggagtca ca 180
tgctaaggca tccttggggc atttgggaaa agngccgctt ggggggtgaga gtgctctagg 240
gccactctgc aatgtccctg gggnccgatg aggtacaaca tgcaccccg ggaccagag 300
gagtggggaa agacatgaag gggatttggg aacagatccg taaaaataa cctgttntgg 360
aaattcacca caggcca 377

```

<210> 69

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 69

```

ttaatttttg aggccgtcca caacttccag gttcccatcc tgcgacttgg tcagcgggtg 60
gaataatctc aagaatcaaa tcatactcct tcccaaagcc tggccacaga aagtcctccc 120
ctgccaagg gaaccgncaa gagagtactg tgtcattcaa tccgtatgag gccaggaact 180
tgcacccggg gcttgcagga caaagggccc cca gaggagg aagccctacc cntgggacac 240

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agaggtgtta cggaggagcc cntacggcgg gacccccgagg gagnttcagg gcccaagggg 300
gtttttactt gggggaccga aag 323

<210> 70

<211> 2541

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2541)

<223> spleen tyrosine kinase (SYK) gene.

<400> 70

gaggaagagc cgcggggcccg gcggtctgagg ccacccccggc ggcggtctgga gagcgaggag 60
gagcggtgtg ccccgcgctg cgcccgccct cgccctcacct ggcgcagggtg g acacctgcg 120
caggtgtgtg ccctccggcc cctgaagcat ggccagcagc ggcattggctg acagcgccaa 180
ccacctgccc ttctttttctg gcaacatcac ccgggaggag gcagaagatt acctggtcca 240
ggggggcatg agtgatgggc tttatttgcg gcgccagagc cgcaactacc tgggtggctt 300
cgccctgtcc gtggccacag ggaggaaggc acaccactac accatcgagc gggagctgaa 360
tgccacctac gccatgcgcg gtggcaggac ccattgccagc ccgcccagacc tctgccacta 420
ccactcccag gactctgatg gcctggtctg cctcctcaag aagcccttca accggcccca 480
aggggtgcag cccaagactg ggccctttga ggatttgaag gaaaacctca tcagggaata 540
tgtgaagcag acatggaacc tgcagggta ggctctggag caggccatca tcagtcagaa 600
gcctcagctg gagaagctga togtaccac agcccatgaa aaaatgcctt ggttccatgg 660
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gacattgcag agtggcctag agcactctca ccccaagcgg ccttttccaa atgcccagg 2400
atgccttagc atgtgactcc tgaagggag gcaaaggcag aggaatttgg ctgcttctac 2460
ggccatgaga ctgatccctg gccactgaaa agctttctctg aca ataaaaa tgttttgagg 2520
ctttaaaaaa aaaaaaaaaa a 2541

<210> 71
 <211> 312
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(312)
 <223> 5' terminal sequence. interleukin 7 receptor
 (IL7R) gene.

<400> 71
 taacatcttt gtaagaaacc aagaaaaaat ttaaagtgtga gtttcaatcc tgaaagtttc 60
 ctggactgcc agattcatag ggtggatgac attcaagcta gagatgaagt ggaaggtttt 120
 ctgcaagata cgtttcctca gcaactagaa gaatctga ga agcagaggct tngaggggat 180
 gtgcagagcc ccaactgccc atctgaggat gtagtcatca ctccaggaaa gctttgggaa 240
 ggagattcat ccctcacatg cctgggctng ggaatgttca gtgcatgtga cgccctatt 300
 tttctccttt t 312

<210> 72
 <211> 1658
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1658)
 <223> interleukin 7 receptor (IL7R) gene.

<400> 72
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 tttacttcaa gtcgtttctg gagaaagtgg ctatgctcaa aatggagact tggaagatgc 120
 agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca 180
 ttactgacc tgtgcttttg aggaccaga tgtcaacacc accaatctgg aatttgaaat 240
 atgtggggcc ctctgtggagg taaagtgcct gaa tttcagg aaactacaag agatataatt 300
 catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttggaga 360
 aaagagtcta acctgcaaaa aaatagacct aaccactata gttaaacctg aggtctcttt 420
 tgacctgagt gtcactctatc gggaaggagc caatgacttt gtggtgacat ttaatacatc 480
 acacttgcaa aagaagtatg taaaagtttt aatgcatgat gtagcttacc gccaggaaaa 540
 ggatgaaaac aaatggacgc atgtgaattt atccagcaca aagctgacac tcctgcagag 600
 aaagctccaa ccggcagcaa tgtatgagat taaagttcga tccatccctg atcactattt 660
 taaaggcttc tggagtgaat ggagtccaag ttattacttc agaactccag aga tcaataa 720
 tagctcaggg gagatggatc ctatcttact aaccatcagc attttgagtt ttttctctgt 780
 cgctctgttg gtcactcttg cctgtgtgtt atggaaaaaa aggattaagc ctatcgatg 840
 gccagtcctc cccgatcata agaagactct ggaacatctt tgtaagaaac caagaaaaaa 900
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 cattcaagct agagatgaag tggaaggttt tctgcaagat acgtttcctc agcaactaga 1020
 agaactctgag aagcagagggc ttggagggga tgtgcagagc cccaactgcc catctgagga 1080
 tgtagtctgc actccagaaa gcttttgaag agattcatcc ctacatgcc tggctgggaa 1140
 tgtcagtgca tgtgaogccc ctattctctc ctcttcagg tccctagact gcaggagag 1200
 tggcaagaat gggcctcatg tgtaccagga cctcctgctt agccttggga ctacaaacag 1260
 cacgctgccc cctccatttt ctctccaatc tggaatcctg acattgaacc cagttgctca 1320

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```
gggtcagccc attcttactt ccctgggato aaatcaagaa gaagca tatg tcaccatgtc 1380
cagcttctac caaaaccagt gaagtgtgtaag aaaccacagac tgaacttacc gtgagcgaca 1440
aagatgattt aaaagggaag tctagagtgc ctagtctccc tcacagcaca gagaagacaa 1500
aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt 1560
cctgagttca gtggcactca acatgagtca agagcatcct gcttctacca tgtggatttg 1620
gtcacaaggt ttaaggtgac ccaatgattc agctattt 1658
```

<210> 73

<211> 236

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(236)

<223> 3' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 73

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taaaaacaat agaaaaaaat caacttttaa aagcaaaatg tacttaaata aaaaaaatta 60
gggttttatag tacctataat actaggnact atatactagg attgaaa ttc tgtgtaactg 120
ctataaacgt tttatttaaag ttattttacat ttaatgggca atatttacag aggaaacatt 180
gtgtaaatct taaaattttt taaaanccaa ttcttaaata ccaaattctgt taaggg 236
```

<210> 74

<211> 413

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial S equence:primer

<220>

<221> misc_feature

<222> (1)..(413)

<223> 5' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 74

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acgtctccac acatcagcac aactacgcag cgccctccctc cactcggaag gactatcctg 60
ctgccaagag ggtcaagttg gacagtgtca gagtcctgag acagatcagc aacaaccgaa 120
aatgcaccag ccccaggtcc tcggacaccg aggagaatgt caagaggcga acacacaacg 180
tcttgggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 240
atcccgaggt tgggaaaaca atgaaaaggc ccccaaggta gttattcctt taa aaaagcc 300
acagcntaca tcctgtttccg ttccaaggca ggagggagcc aaaagttcat tttnttgaag 360
gagggntttt ttttccgggn aacgacgagg aaccattttt aaacacaant ttt 413
```

<210> 75

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

53/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene
homolog (MYC) gene.

<400> 75

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ctgctcgcg cgcaccgc cgggccccg cgtccctgg ctccctcct gcctcgagaa 60
gggcagggt tctcagagg ttggcggga aaaagaacg g agggaggat cgcgtgagt 120
ataaaagccg gttttcggg ctttatctaa ctgctgtag taattccagc gagaggcaga 180
gggagcgagc gggcgcccg ctaggggtga agagccggc gagcagagct gcgctgcggg 240
cgtcctggga agggagatcc ggagcgaata gggggcttcg cctctggccc agccctccc 300
cttgatcccc caggcca gcg gtccgcaacc cttgccgat ccacgaaact ttgcccatag 360
cagcgggcg gcactttgca ctggaactta caacaccga gcaaggacgc gactctccc 420
acgcggggag gctattctgc ccatttgggg acacttcccc gccgctgcca ggaccgcgtt 480
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cagcagcctc ccgcgacgat gcccctcaac gttagcttca ccaacaggaa ctatgacctc 600
gactacgact cgggtgcagc gtattttctac tgcgacgagg aggagaactt ctaccagcag 660
cagcagcaga gcgagctgca gcccccgcg ccagcgagg atatctggaa gaaattcag 720
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gttgcggtca cacccttctc ccttcgggga gacaacgacg gcggtggcg gagcttctcc 840
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tctgaagagg acttggttgc gaaacgacga gaacagttga aa cacaact tgaacagcta 1860
cggaactctt gtgcgtaagg aaaagtaagg aaaacgattc cttctaacag aaatgtcctg 1920
agcaatcacc tatgaacttg tttcaaatgc atgatcaa at gcaacctcac aaccttggt 1980
gagtcctgag actgaaagat ttagccataa tgtaaaactgc ctcaaattgg actttgggca 2040
taaaagaact tttttat gct taccatctt ttttttctt taacagattt gtatttaaga 2100
attgttttta aaaaatttta a 2121

```

<210> 76

<211> 260

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(260)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

54/292

<400> 76

```

tcacagcact agagaccctg ttaaataggg gatatgagtc agaatggctt attcacagat 60
ggggtccaga ttcagtgggt ggaacacaga caccacagtg agctcctttg caaagtggca 120
aacataatth tgctttctgc cttcaaaaac atatatccat cgcgtttagg cttcatgata 180
ctgctcctgc aaaaatgcaa gtcgaaaggg actgcagggg ctctcgctgg ggggccctgt 240
gagcatcgag cagggtctct 260

```

<210> 77

<211> 409

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(409)

<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 77

```

cattctgggt catagatggc atcttttcac tgtgtttctca cattgggtgga aaggaagaac 60
tctggtttct tcacttcctt ataagggcac caatcttatt caccaggggt tcaccctcga 120
aataatcacg tcctcaaaaac cccacacctt taatatctta ataccatcac gtgaggggct 180
aggtttcaac ataagaattc ggtgggtggtt ggggttngggg gagagggaaa caaacatcca 240
gaccagaaac cgaaaaatgt ctagcaaata caaaaagtgc aaaaaagt gc atgactcact 300
ggaggacttc cccaagganc agctnctgtt taaccggggc cgcccttttc caggacacat 360
gttccttccc tggnggccac atnttgnnc ttnaggccan tccagggca 409

```

<210> 78

<211> 2365

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2365)

<223> gata-binding protein 3 (GATA3) gene.

<400> 78

```

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ccggcgagag ggcgcgacga cagccgagga catggagggt acggcggacc agccgcgctg 180
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cctcagccac tcctacatgg acgcggcgca gtaccgcgtg ccggaggagg tggatgtgct 300
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cacggtgcag aggtaccctc cgaccacca cgggagccag gtgtgcgcgc cgcctctgct 420
tcatggatcc ctaccctggc tggacggcgg caaagccctg ggcagccacc acaccgcctc 480
cccttgaat ctcagccctt tctccaagac gtccatccac caccgctccc cggggccctt 540
ctcgtctac ccccggcct cgtcctcctc cttgtcgggg ggccacgcca gcccgcacct 600
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aggctcgccc ggctaggccc ggcaggacga gaaagagtgc ctcaagtacc aggtgcccc 720
gcccagacgc atgaagctgg agtcgtccca ctcccgctgg agcatgaccg cctgggtgg 78 0
agcctcctcg tcgaccacc accccatcac cacctaccgc ccctacgtgc ccgagtacg 840
ctccggactc tccccccca gcagcctgct gggcggtctc cccaccggct tcggatgcaa 900

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55/292

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gtccaggccc aaggcccggt ccagcacagg cagggagtgt gtgaactgtg gggcaacctc 960
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tcacaaaatg aacggacaga accggccctt cattaagccc aagcgaaggc tgtctgcagc 1080
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ttatcacagc cgaactgttg tataaattta tttactgcta gtcttaagaa ctgctttctt 2280
tcgtttgttt gtttcaa tat tttccttctc tctcaatttt cggttgaata aactagatta 2340
cattcagttg gcaaaaaaaaa aaaaa 2365

```

<210> 79

<211> 328

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(328)

<223> 3' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 79

```

ttgtatnttt naaataatct ttattgtcac tagtataaaa cagagcagat caactggcct 60
ctcggctctgt acaaagtgtg gggcgtgaaa ccgctgggct gccccactt ctcccataat 120
tccctgccct agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtggggg ctgttttcta tctgaggagg 240
gcaaagaagc agaggagaaa actggagtgg cggaaacctc ccgntcctca tcccgtcccc 300
tgtggccgat cccanagtc actnggat 328

```

<210> 80

<211> 428

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(428)

<223> 5' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 80

```

ggctccccac ccttgagaag tgcctcagat aataccctgg tggccatgga cttctctggc 60
catgctgggc gtgtcattga gaacccccgg gaggctctga gtgtggccct ggaggaggcc 120
caggcctgga ggaagaagac aaaccaccgc ctcagcctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctggttcca cgggcgcatt tcccgtgagg 240
agagccagcg tttattggga cagcagggtc tngtagacgg cctgttcctg ggtccgggag 300
agtcagcggg aacccccagg ggtttttcct ctttttnttg ccaccttgca gaaagtgaag 360
cnttattttc attccttgcc gagcgaagga ggaaggggcc cttttatttt aagcattggg 42 0
tgattggc 428

```

<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7
(GRB7) gene.

<400> 81

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cacagggtct cccccgcct ctgactttct tgtccgaagt cgggacaccc tcctaccacc 60
tgtagagaag cgggagtggg tctgaaataa aatccaggaa tctgggggtt cctagacgga 120
gccagacttc ggaacgggtg tctgtctact cctgctgggg ctctccagg acaaggga c 180
acaactgggt cegttaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
cctcatctta gcagctctcc ggaagacctt tggccagccc ctgggacccc tcctgggact 300
ccccggcccc ctgatacccc tctgcctgag gaggtaaaga ggtcccagcc tctcctcatc 360
ccaaccaccg gcaggaaact tcgagaggag gagaggc gtg ccacctccct cccctctatc 420
cccaacccct tccctgagct ctgcagtcct cctcaccaga gcccaattct cgggggcccc 480
tccagtgcaa gggggctgct cccccgcgat gccagccgcc cccatgtagt aaagggtgtac 540
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tgccaccccc acctagcact ggagcggggt ttggaggacc acgagtccgt ggtggaagtg 720
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tacgaactgt tcaagagctc cccacactcc ctgttcccag aaaaaatggt ctccagc tgt 840
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acgcgggtgg ccctctgacc aggcggtgga ctggctcatg cctcagccc ccttcaggct 1860
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ggagcgggag ggttcgcgca ctccagtttt ctctctgtct tctttgcctc cctcagatag 1980
aaaacagccc ccactccagt ccactcctga cccctctcct caagggaagg ccttgggtgg 2040
ccccctctcc ttctcctagc tctggagggt ctgctctagg gcagggaatt atgggagaag 2100
tgggggcagc ccaggcggtt tcacgcccc cacttt gtac agaccgagag gccagttgat 2160
ctgctctggt ttatactagt gacaataaag attatttttt gatac 2205
```

<210> 82

<211> 313

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii
beta (180kd) (TOP2B) gene.

<400> 82

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gaaatttgac agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa 60
acagacagat aaagttccaa gtaaaacggt agctgctaaa aagggtatgt acttatattt 120
gattgagtta agcattgg at agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180
actatttgca tttttttatc ataaaacaat taagggaagta taagtgttta taaggaggac 240
ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta ntttaaagct 300
gttggtanttt taa 313
```

<210> 83

<211> 4866

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)
gene.

<400> 83

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acctgggtga acaatgctgc aaaaaaagaa gagtcagaaa ctgccaaaca aaatgattct 120
tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180
cttcgtcctg atacatatat tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240
gatgaagatg taggaatgaa ttgcagggtg gttacotttg tgccaggttt atacaagatc 300
tttgatgaaa ttttggttaa tgctgctgac aataaacaga gggataagaa catgacttgt 360
attaaagtgt ctattgatcc tgaatctaac attataagca tttggaataa tgggaaaggc 420
attccagtag tagaacacaa ggtagagaaa gtttat gtcc ctgctttaat ttttggacag 480
cttttaacat ccagtaacta tgatgatgat gagaaaaaag ttacagggtg tcgtaatggt 540
tatggtgcaa aactttgtaa tattttcagt acaaagttta cagtagaaac agcttgcaaa 600
gaatacaaac acagttttta gcagacatgg atgaataata tgatgaagac ttctgaagcc 660
aaaatttaag attttgatgg tgaagattac acatgcataa cattccaacc agatctgtcc 720
aaattttaaga tggaaaaact tgacaaggat attgtggccc tcatgactag aagggcata 780
gatttggtcg ttctgtgtag aggggtcaag gtcatgttta atggaaagaa attgcctgta 840
aatggatttc gcagttatgt agatctttat gtgaaagaca aattggatga aactgg ggtg 900
gccctgaaag ttattcatga gcttgcaaat gaaagatggg atgtttgtct cacattgagt 960
```

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aacaaagctg	gtgtatcagt	gaaaccattt	ca agtaaaaa	accatatatg	ggttttttatt	1140
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tcagaatttg	gc attccaaa	gaagactaca	acacccaaaag	gtaaaggccg	agggggcaag	4620

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```

aaaaggaaag catctggctc tgaaaatgaa ggcgattata accctggcag gaaaacatcc 4680
aaaacaacaa gcaagaaacc gaagaagaca tcttttgatc aggattcaga tgtggacatc 4740
ttcccctcag acttccctac tgagccacct tctctgccac gaaccggctg g gctaggaaa 4800
gaagtataat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860
aattaa                                     4866

```

<210> 84

<211> 311

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(311)

<223> 3' terminal sequence. caspase 4,
apoptosis-related cysteine protease (CASP4) gene.

<400> 84

```

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aagttgatta aggagggtg ggctgcttgt ggcttccatt ttcaattgcc aggaaagagg 120
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gtttcaaatg attgctgtac ctcccgaaat acttctctta ggtggcagca ccaagaatat 240
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cagggcacgt t                                     311

```

<210> 85

<211> 1291

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1291)

<223> caspase 4, apoptosis-related cysteine
protease (CASP4) gene.

<400> 85

```

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gaaaaaagcc acttaaggtg ttggaatccc tgggcaaaga ttctctcact ggtgttttgg 120
ataacttggg ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180
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aagctcatcc gaatatggag gctggaccac ctgagtcagg agaatctaca gatgccctca 360
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tcatgtctca tggcatcctg gagggaaatc gcggaactgt gcatgatgag aaaaaaccag 720
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aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgctttc tgctcttcaa 960

```

60/292

```
cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcac acacaactca 1020
tcacatgctt ccagaaatat tcttggtg ct gccacctaga ggaagtattt cggaaggtac 1080
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tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
cctccttaat caacttcaag gagcaccttc attagtacag cttgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaaa a 1291
```

<210> 86

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 86

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ccagtcgaaa cccttgagg ctttttttgc agttggccac aggggcgttg gaggcctgct 120
tatgggtcct cgatgtcgag aaactoctgc ttgngggaac ccgcg ccgcg tnnccacgca 180
caggagccnt cacttctctt gatgcaggcg aagaacttgg cctggnnccc gttnatgttc 240
ttctctgtga ccagtcctat ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
atngggcanc gcgtgatct 319
```

<210> 87

<211> 1075

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1075)

<223> tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 87

```
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gccgcccccc acccgccgc cccgcccggc gaattgcgcc ccgcgccct cccctcgcg 120
ccccgagaca aagaggagag aaagtttgcg cggccgagcg gggcaggtga ggagggtag 180
ccgcgcggga ggggcccgc tcggcccccg ctcagcccc gcccgcgccc ccagcccgc 240
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tctcgctgga cgttggagga aagaaggaat atctcattgc aggaaaggcc gagggggacg 660
gcaagatgca catcaccctc tgtgacttca tcgtgccc tg ggacaccctg agcaccaccc 720
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ccatgatccc gtgctacatc tcctccccgg acgagtgcct ctggatggac tgggtcacag 840
agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900
```

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cctgtgctgtg gtaccg cggc gcggcgcccc ccaagcagga gtttctcgac atcgaggacc 960
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020
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<210> 88
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(225)
<223> 3' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 88
ttttttgaat gaggaagctc tcttcatttta tttcanatga ggatgaagaa gaggattatg 60
tgancacagg aatnttgcag ggggataat ccaaagctgg ttatctccag gncctcantn 120
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat ccctccgtgc 180
ccaatcataa aaaagtcagt accgtcccta tnttgccaat ntgcc 225

<210> 89
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 89
cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcggnn tngagaaac 60
gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg aacgtgacgg 120
tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg cagtgttcca 180
tctcctccat cggcgtagtg gggcaccgag agggacaacc gcagccacag cgccatttc 240
ttttgagttt tttcaccaag gagctaagcc cctgccaggg acccgat ant tattccnttt 300
ttttcccttt gg 312

<210> 90
<211> 666
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(666)
<223> d-dopachrome tautomerase (DDT) gene.

<400> 90

```
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cccgccatgc cgttcctgga gctggacacg aatttgccc ccaaccgagt gcccgcgggg 180
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cagctgtcca tctcctccat cggcgtagtg ggcacgcgg aggacaaccg cagccacagc 360
gccactttct ttgagttttc caccaaggag ctagccctgg gcc aggaccg gatacttata 420
cgctttttcc ccttgagatc ctggcagatt ggcaagatag ggacggtcac gactttttta 480
tgattgggca cggagggatc cagggcatct gtgaactggc tgcttcttcc agagagatct 540
cttggcagag tgagggcctg gagataacca gctttggatt atcccgcacg caacattcct 600
gtgatcacat aatcctcttc ttcacctca tatgaaataa atgaagagag cttcctcatt 660
caaaaa
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<210> 91

<211> 443

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(443)

<223> 3' terminal sequence. prolactin (PRL) gene.

<400> 91

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gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60
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cttctcagaa atagatgaaa tggatgtggg ctttagca gtt gttggtgtgg atgattcggg 180
cacttcaggg agcttgagga taattgtcga ttttatgtga atccctgcgt aggcaatggg 240
agagggtata ataaggcagg aaagggcgag actcttcac agccatctgc aggggatggg 300
aagtccccga ccagacagg gtagatctca ttttctttgg gttttcaggg atgaacctgg 360
gcttgactat ccagcttcca tgnccctctt ggaagccctt ttgggtttgc tccctcaatc 420
ttctacagct tttgggttag ggt
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<210> 92

<211> 243

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(243)

<223> 5' terminal sequence. prolactin (PRL) gene.

<400> 92

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gaagaatcgg aacatacagg ctttgatata aaaggtttat aaagccaata tctgggaaag 60
agaaaaccgt gagacttcca gatottctct ggtgaagtgt gtttcctgca acgatcacga 120
acatgaacat caaaggatcg ccatgggaaa gggctccctcc tgctgctgct ggggtgttcaa 180
acctgctect gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240
gat
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<210> 93
<211> 833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(833)
<223> prolactin (PRL) gene.

<400> 93
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cctgctgctg tgccagagcg tggcccccctt gcccatctgt cccggcgggg ctgcccgatg 12 0
ccagggtgacc cttcagagacc tgtttgaccg cgccgtcgtc ctgtcccact acatccataa 180
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gaatgagcct ctgtatcatc tggtaacgga agtacgtggt atgcaagaag ccccgagggc 420
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gctgatagtc agccagggtc atcctgaaac caaagaaaat gagatctacc ctgtctggtc 540
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ccgaatcatc cacaacaaca actgctaagc ccacatccat ttcattctatt tctgagaagg 720
tccttaatga tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780
tgggtgtaac aggtctcctc ttaaaaaata aaaactgact cgttagagac atc 833

<210> 94
<211> 304
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(304)
<223> 3' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 94
actaagcagt gtgcttttat ttcattgaac acatagtttt ataactaaca gcaaaaagta 60
aatctacaaa tcacagttag gaaacataat gatttgttct ggaatcagct gctggagaaa 120
gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gcttttagtag tgtcagtctg 180
actacattct tgaggcattt caggtactct gtagtggtac ctgaagaaaa atcacatttt 240
aaccaatcat tccattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300
cggg 304

<210> 95
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(366)
 <223> 5' terminal sequence. prolactin receptor
 (PRLR) gene.

<400> 95
 gaggtcattg agaagccaga gaatcctgaa acancccaca cctggaaccc ccantgcata 60
 agcatggaag gcaaaatccc ctatttncat gctgggtggat ccaaattgttc aacatggccc 120
 ttaccacagc ccagccagca caaccccaga tcctcttacc acaatattac tgatgtgtgt 180
 gagctggctg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240
 gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300
 ggaggtagga aagcttccat tcttgagnac tgaccagggt tacgncctgg gttgcttgcc 360
 ccaggg 366

<210> 96
 <211> 2723
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2723)
 <223> prolactin receptor (PRLR) gene.

<400> 96
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 atgtcctcgt gcaggaagta ctcatcgact gatgtggcag actttgctcc ctgacaaaac 180
 taaagaactc tcctattcat ggaggcgaac actgaggatg ctttccacat gaaccctgaa 240
 gtgaacttct gatacatttc ctgcagcaag agaaggcagc caacatgaag gaaaatgtgg 300
 catctgcaac cgttttccact ctgctacttt ttctcaac ac ctgccttctg aatggacagt 360
 tacctcctgg aaaacctgag atcttttaaat gtctgttctcc caataaggaa acattcacct 420
 gctggtggag gcctgggaca gatggaggac ttcctaccaaa ttattcactg acttaccaca 480
 gggaaggaga gacactcatg catgaatgtc cagactacat aaccggtggc cccaactcct 540
 gccacttttg caagca gtac acctccatgt agaggacata catcatgatg gtcaatgcca 600
 ctaaccagat gggaagcagt ttctcggatg aactttatgt ggacgtgact tacatagtcc 660
 agccagaccc tcctttggag ctggctgtgg aagtaaaaaca gccagaagac agaaaacctt 720
 acctgtggat taaatggtct ccacctaccc tgattgactt aaaaactggt tggttcac gc 780
 tcctgtatga aattcgatta aaaccogaga aagcagctga gtgggagatc cattttgctg 840
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 ctgaccagga tacgccttgg ctgctgcccc aggagaaaac cccctttggc tccgctaaac 1800
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aacagagaga gaacagcggc aagcccaaga agcccgggac tcctgagaac aataaggagt 1920
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ctaaaaacgt ggcttgcttt gaagaatcag ccaaagaggc cccaccatca cttgaacaga 2040
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tgggtggttt ggattacctg gatcccgcat gttttacaca ctccctttcac tgatagcttg 2160
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<210> 97

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 97

```

gtacagttac cttttattta tagcgaaaat gggttttttc atttacagag taacaaagat 60
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aagtggggga agggcaaata caatttcctt ttgggggggg atagggngac ccccttttgc 300
gagaggggtt aggtgggggt tccccccggn acacacaggc aagggttttg gngccccttg 360
tgggg                                     365

```

<210> 98

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(366)

<223> 5' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 98

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nattcggcac tagggggcac ctgaccacac gccccacag gctctgacca gcagcctatg 60
agggggtttg gcaccaagct ctgtccaatc aggtaggctg ggctgaacta gccaatcaga 120
tcaactctgt cttgggcgtt tgaactcagg gagggaggcc cttgggagca ggtgcttg 180
gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttgg gttcccaata caaaaatacc tactgctgag aggggntgct gaccattttg 300

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gtcaaggatt tcngtttgcc ttatatccca aataaantcc cttttttttn aggttttntt 360
 agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

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 tgcccctggc tacctcttgg gcatctgcag cggatgaatg cacttcccag ttcacatgct 240
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 aactgaccac agttgacatc gtcaccctga ggggtgctgt ccgtgagggg gtgcgatgga 480
 ggggtgatggc catc caggac ttcaagccct ttgagaacct tcgcctgatg gcccctatct 540
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 cctcccacta ctttgaaaga cacctggagt tcgagggccg gacgctgtcc ccaggccaca 660
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aaaataagta caat 4034

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<210> 100

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(444)

<223> 3' terminal sequence. gata -binding protein 3
(GATA3) gene.

<400> 100

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tttctatttt tttattttct tttaatgcat caaacaactg tggccagtga aaggaaacaa 60
aactggcagt ttgtccattt gaatatcaga cctagtttct tcttaatttc cactacta ttt 120
ctcccatatt ccttaaactt cttggcatcc ttcattgcctt acagctaccc agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggctcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggtg 360
aggctccctt tgccaaagggt ggggccaac ataattttgg cttttctggc cttcaaaaa 420
catatttccn tcgcgttttg gggg 444

```

<210> 101

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(396)
<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 101
gcaatgggga cctgtctgc aatgcctgtg gntctactac aagcttcaca atattaacag 60
acccttgact atgaagaagg aaggcatcc a gaccagaaac cgaaaaatgt ctagcaaadc 120
caaaaagtgc aaaaagtgc tgactcactg gaggacttcc ccaagaacag ctcgtttaac 180
ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240
agccacatgc tgaccacggc ccacgccgat ggcaccogcc atccagcctg tcctttggga 300
ccacaccacc cctccagctg ggtcaccgcc ntgggttttag agccttgtn gatggttcac 360
agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. placental growth
factor, vascular endothelial growth factor -related
protein (PGF) gene.

<400> 102
attcgacact aggggagacc caagggcagg gggaagagga ggagagagaa gcagagaccc 60
acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaccctc tggaggagag 120
agaccccgca cccggctcgt gtatttatta ccgtcacact cttcagtgc tcctgctggt 180
acctgccctc tatttattag ccaactgttt ccctgctgaa tgccctcgctc cttcaagac 240
gaggggcagg gaaggacagg accctcagga attcagtgcc ttcaacaacg tga gagaaag 300
agagaagcca gccacagacc cctggggagc tttccgcttt tgaaagaagc aagacaagtt 360
ggccttggtg aggggcaagg ttagggccca ggaggccctn gggaagtttt tcaggg 416

<210> 103
<211> 1645
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1645)
<223> placental growth factor, vascular
endothelial growth factor-related protein (PGF)
gene.

<400> 103
gggattcggg ccgcccagct acgggaggac ctggagtggc actgggcgcc cgacggacca 60
tccccgggac ccgctgccc ctoggcgccc cgccccgccc ggccgctccc cgtcgggttc 120
ccagccaca gccttaccta cgggctcctg actccgcaag gcttccagaa gatgctcgaa 180
ccaccggccg gggcctcggg gcagcagtga gggaggcgtc cagcccccca ctcagctctt 240
ctcctcctgt gccaggggct ccccggggga tgagcatggt gggtttccct cggagcccc 300

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tggctcggga cgtctgagaa gatgccggtc atgaggctgt tcccttgctt cctgcagctc 360
ctggccgggc tggcgtgcc tgctgtgccc cccagcagt gggccttgct tgctgggaac 420
ggctcgtcag aggtggaagt ggtacccttc caggaagtgt ggggccgcag ctactgccgg 480
gcgctggaga ggctggtgga cgtcgtgtc c gagtacccca gcgaggtgga gcacatgttc 540
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tgtgtgccgg tggagacggc caatgtcacc atgcagctcc taaagatcog ttctggggac 660
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gggaggagcc tgtgcgtccc agctgaaggc agtggcaggg gagcaggttc cccaagggcc 1560
ctggcaccct cacaagctgt ccctgcaggg ccactctga ct gccaaagccag attctcttga 1620
ataaagtatt ctagtgtgga aacgc 1645

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<210> 104

<211> 309

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(309)

<223> 5' terminal sequence. ubiquitin protein
ligase e3a (human papilloma virus e6 -associated
protein, angelman syndrome) (UBE3A) gene.

<400> 104

```

ttcgcanag gggaaatgaa gcctgcacga atgagttttg tgcttcctgt ccaacttttc 60
ttcgtatgga taataatgca gc agctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aaggtgcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
ttggatttta aagatgtgac ttactttaac aggaaggagg aagggtatta tggaaaattt 300
tctttggac 309

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<210> 105

<211> 2628

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2628)

<223> ubiquitin protein ligase e3a (human

papilloma virus e6-associated protein, angelman
syndrome) (UBE3A) gene.

<400> 105

```
atggagaagc tgcaccagtg ttatttgaaa tcaggagaac ctcagtctga cgacattgaa 60
gctagccgaa tgaagcgagc agctgcaaag catctaatag aacgctacta ccaccagtta 120
actgagggct gtggaaatga agcctgcacg aatgagtttt gtgcttcctg tccaactttt 180
cttcgtatgg ataataatgc agcagctatt aaagccctcg agctttataa gattaatgca 240
aaactctgtg atcctcatcc ctccaagaaa ggagcaagct cagcttacct tgagaactcg 300
aaagggtgcc ccaacaactc ctgctctgag ataaaaatga aca agaaagg cgctagaatt 360
gatttttaag atgtgactta cttaacagaa gagaagggtat atgaaattct tgaattatgt 420
agagaaagag aggattattc ccctttaatc cgtgttattg gaagagtttt ttctagtgtc 480
gaggcattgg tacagagctt cgggaaagtt aaacaacaca ccaaggaaga actgaaatct 540
cttcaagcaa aagatgaaga caaagatgaa gatgaaaagg aaaaagctgc atgttctgct 600
gctgctatgg aagaagactc agaagcatct tcctcaagga taggtgatag ctacacggga 660
gacaacaatt tgcaaaaatt aggcctgat gatgtgtctg tggatattga tgccattaga 720
agggctctaca ccagattgct ctctaataaa aaaattgaaa ctgcctttct caatgcactt 780
gtatatttgt cacctaactg ggaatgtgac ttgacgtatc acaatgtata ctctcgagat 840
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gagacatttc agcaacttat tacttataaa gtcataagca atgaatttaa cagtcgaaat 1080
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gcaaatgtag tgggagggga agtggacaca aatcacatg aagaagatga tgaagagccc 1200
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gagatgatcg ctatggaaaa tcctgcagac ttgaagaagc agttgtatgt ggaatttgaa 1680
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ggaagccgga atctagat tt ccaagcacta gaagaaacta cagaatatga cgggtggctat 2340
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cagaaaagac tcttcttgca gtttacaacg ggcacagaca gagcacctgt gggaggacta 2460
ggaaaattaa agatgattat agccaaaaat ggccagaca cagaaagggt acctaca tct 2520
catacttgct ttaatgtgct tttacttcog gaataactca gcaaagaaaa acttaaagag 2580
agattgttga aggccatcac gtatgccaaa ggatttggca tgctgtaa 2628
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<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 106
aattttaatt ctagcacctg aagctataca agggatgct ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgcttaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagttata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagncgg ggnatactgg aaagtggatt tcagnggtct catcctgttg gtactctatt 300
gggggngggg ttcttgaggt aggttatggt ggact gggnc caaggntggg ggggtaccacc 360
cag 363

<210> 107
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(408)
<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 107
gaattgaatc tacaaaagtg aaccatctca gacctttact gatactacaa cttttgtttt 60
ctgatggcca aaataccaaa tgcctgttgt atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctactc ttggagatga taatatct ta tgtgggtcaaa tatttggact 180
catttaggac ttagatattt cagtgtactt gattttttta ttttaactctt tttcacagcc 240
acgctaaggg taaaaaggaa taatttcctt ctgtcttctt tttcaagtat ttctgggtaa 300
gggattcaaa aaactaaaac tgtttttgtt tgtaatatata aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgntt 408

<210> 108
<211> 612
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(612)
<223> oncogene tc21 (TC21) gene.

<400> 108
atggccgcgg cggctggcgg acggctccgg caggagaagt accggctcgt ggtggtcggc 60
gggggcggcg tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttgtaacg 120
gattatgac caaccattga agattcttac acaaagcagt gtgtgataga tgacagagca 180
gcccggttag atatttttga tacagcagga caagaagagt t tggagccat gagagaacag 240
tatatgagga ctggcgagg ctctctgttg gtcttttcag tcacagatag aggcagtttt 300
gaagaaatct ataagtttca aagacagatt ctacagagtaa aggatcgtga tgagttccca 360
atgattttta ttggtataaa agcagatctg gatcatcaaa gacaggtaac acaggaagaa 420
ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcctc cttcaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600

gtcattttct ag

6 12

<210> 109
 <211> 592
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(592)
 <223> 5' terminal sequence. tyrosine kinase with
 immunoglobulin and epidermal growth facto r
 homology domains (TIE) gene.

<400> 109
 ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60
 ttatgtgaag aagacgatgg ggcgtctccc tgtgcgctgg atggccattg agtccctgaa 120
 ctacagtgtc tataccacca agagtgatgt ctggtccttt ggagtccttc ttggggagat 1 80
 agtgagcctt ggaggtacac cctactgtgg catgacctgt gccgagctct atgaaaagct 240
 gccccagggc taccgcatgg agcagcctcg aaactgtgac gatgaagtgt acgagctgat 300
 gcgttcagtg ctggcgggac cgtccctatg agcgaccccc ctttgcccag attgcgctaa 360
 cagctagggc gcatgctggg aagccagggg aggcctatgt gaacatgttc gctgtttgag 420
 aacttcaatt aacgcgggca ttgatgccac agctgaggag gnctgagctg ccatccagcc 480
 agaactnggt ctgttggccg gagcaaattt ggtgtctaaa ctgtgaccag ttnaacctta 540
 aagctttgat ttaagttgct taaggatttt tttaattaag ggagaaaaat tt 592

<210> 110
 <211> 3845
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(3845)
 <223> tyrosine kinase with immunoglobulin and
 epidermal growth factor homology domains (TIE)
 gene.

<400> 110
 cgctcgtcct ggctggcctg ggtoggcctc tggagtatgg tctggcgggt gccccctttc 60
 ttgctcccca tcctcttctt ggcttctcat gtgggcgcgg cgggtggacct gacgctgctg 120
 gccaacctgc ggctcacgga cccccagcgc ttcttcctga cttgcgtgtc tggggaggcc 180
 ggggcgggga ggggctcgga cgctggggc cc gccccctgc tgetggagaa ggacgaccgt 240
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 ccagacaagg tcacacacac tgtgaacaaa ggtgacaccg ctgtactttc tgcacgtgtg 480
 cacaaggaga agcagacaga cgtgatctgg aagagcaacg gatcctactt ctacaccctg 540
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 tcgagcggca tctacagtgc cacttacctg gaagccagcc ccctggggcag cg ccttcttt 660
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 ccaggttgcc tacatggagg tgtctgccac gaccatgacg gcgaatgtgt atgccccct 780
 ggcttcactg gcaccgcgtg tgaacaggcc tgcagagagg gccgttttgg gcagagctgc 840

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caggagcagt gccagggcat atcaggctgc cggggcctca ccttctgcct cccagacccc 900
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aaccgaggtt acttgatat cgctattgaa tatgccccct acgggaacct gctagatttt 2 820
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gagaacctag cctccaagat tgcagacttc ggcctt tctc ggggagagga ggtttatgtg 3060
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cttaagctgc ctcaaggaat ttttttaact taaggagaa aaaaaggat ctggggatgg 3600
ggtgggctta ggggaactgg gtcccatgc tttgtagggt tctcatagct atcctgggca 3660
tccttctttc tagttcagct gccc cacagg tgtgtttccc atcccactgc tcccccaaca 3720
caaaccccca ctccagctcc ttcgcttaag ccagcactca caccactaac atgccctgtt 3780
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aaaaa

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384 5

<210> 111

<211> 202

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(202)
 <223> 3' terminal sequence. autocrine motility
 factor receptor (AMFR) gene.

<400> 111
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 ccacaggct ttagcactgc ctaatttact tcaccaatga atgaaaacca taaaccaaag 120
 cttgctgcct aaccactccc cagggccaga cgggacaagg aaatgctgag aggggagggg 180
 acccatgggg canantnatg ag 202

<210> 112
 <211> 450
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(450)
 <223> 5' terminal sequence. autocrine motility
 factor receptor (AMFR) gene.

<400> 112
 attcaagtac cttttcctac acagcgggtca gatagcatca gacctgcatt gaacagtcct 60
 gtggaaaggc caagcagtga ccaggaagag ggagaaactt ctgctcagac cgagcgtgtg 120
 ccactggacc tcagtcctcg cctggaggag acgctggact tcggcgagggt ggaagtggag 180
 ccagtgagg tggaagactt cgaggctcgt gggagcgtt tctccaagtc tgctgatgag 240
 agacagcgca tgtggtngca gcgtaaggac gaactcctcc agcaagctcg caaacgtttt 300
 cttgaacaaa agttctgaag atgatgccgg ccttcagaga gctttcctnc ccttcggaaa 360
 ggtgccgttc cttttgaacc ccgtgaaccc ctgnogttcg aaaggattgc ttggcttgcc 420
 cgccgcggga aacggaggct ttcagaagca 450

<210> 113
 <211> 1810
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1810)
 <223> autocrine motility factor receptor (AMFR)
 gene.

<400> 113
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 gccactggac ctcagtcctc gcctggaggga gacgctggac ttcggcgagg tggaagtgga 120
 gccagtgag gtggaagact tcgaggctcg tgggagcgc ttctccaagt ctgctgatga 180
 gagacagcgc atgctggctg cagcgtaagg acgaactcct ccagcaagct cgcaaacgtt 240
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 cgtcctctga ccccgtagac ctgcgtcgaa ggatgctggc tgccgcgcgg aacggagggt 360
 tcagaagcag cagacctcct agcgctccct tgccctctc agctgcct cc tgcgccctgt 420
 gcccgactga ctggaggagg cctgtcccaa ttctgcgcgt ccattggaaaa gcgggcttga 480

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ctgcattgcc gctgtataaa gcatgtgggc ttatagtgtt tggacagctg ataaatttaa 540
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cggaaagtgt ttagaatgtt gaaaagtaat tgaaaaaggt gataggtaaa ttttaggca 1680
aagataattt atttcaataa atctttcaaa agc cttacct tgaaatgctg ttagtaaat 1740
tctgtgcatt tttttttttt aatttgtttt gctgagagca tagctatttg tttttattgt 1800
aaacccgccc                                     1810

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<210> 114

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;
cdna dkfzp434c136 (from clone dkfzp434c136) (EST
R81127) gene.

<400> 114

```

gaaattccaa aatcactcta gtttattcac ataatatagn atttgattcc attcttttgn 60
actgtntccn actttttacaa tgtgtacaat gtttcaccat gtnccaatta atgggtgagc 120
tttaaatgaa aatattcttg ancttccatt tatnggnatc aaccacaata gcaagacccc 180
cangaaatac ttgatctaaa ctgggagggt ccaacacaat tttttttttt aatgggnctt 240
gccacctt                                     248

```

<210> 115

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 3' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

```

<400> 115
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caaagttaat acagataaat ggtatataat gcaataatgc cacagagtta ttccatcaat 120
gtttcanggc tgattctaaa ctggangaaa aaaaaaattn cctagtttat ttgctganga 180
tgtcacttct tttgttactt ctttatagtt ccccaccatt gattnntttt ttaatgcccc 240
ggggtgtaca ggataacccc catattccac accggggnac ttttttttg tcaggggttt 300
caaataaanc caaactacag tgacaggata atgttttaca ggtaattccn tgggccgggg 360
ggtcaattat ncctggacac ctcacttcaa ggcntccttt gggggttttg gggcc 415

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```

<210> 116
<211> 468
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

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<220>
<221> misc_feature
<222> (1)..(468)
<223> 5' terminal sequence. b-cell cl1/lymphoma 2
      (BCL2) gene.

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```

<400> 116
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gagtaagaaa cagaatcctc tggaacttga ggaagtgaac atttcggtga cttccgcac 180
aggaaggcta gagttaccca gagcatcagg cgcgccaaag tgcctgcttt t aggagaccg 240
aagtccgcag aacctgcctn tgtcccagct tggaggcctg gtcctgggaa ctgagccggg 300
gccctcactn gcctcctcca gggatgatca acaggngcag tgtggtntcc gaatgtctgg 360
aagcttgatg ggagctcaga atttccactg ttcaagaaag agncagtaga ggggtgtngc 420
tgggncgtgt cacctggggg ccctncaggt agngcccntt tttcacgt 468

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```

<210> 117
<211> 6030
<212> DNA/RNA
<213> Artificial Sequence

```

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<220>
<223> Description of Artificial Sequence:primer

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<220>
<221> misc_feature
<222> (1)..(6030)
<223> b-cell cl1/lymphoma 2 (BCL2) gene.

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```

<400> 117
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taaccgggag atagtgatga agtacatcca ttataagctg tcgcagaggg gctacgagtg 120
ggatgcggga gatgtgggag ccgcgcccc gggggccgcc cccgcgccgg gcatcttctc 180
ctcgcagccc gggcacacgc cccatacagc cgcattccgg gacccg gtcg ccaggacctc 240
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<210> 118

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian
erythroblastic leukemia viral oncogene homolog 2
(neuro/glioblastoma derived oncogene homolog)
(ERBB2) gene.

<400> 118

```

caaggggctg caaactnncc cacacatgac ccagccctc tacagcggtg cagtgaggac 60
cccacagtac ccttgccctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cggccccagc ccct tcgcc ccgagaggcc 180
ctctgcctgc tgcccgcct gctggtgcca ctctggaaag gcccaagact ctctcccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc ctttgggggt gccgtgggag aaccccgagt 300
attgacaccc caggggaggg agcttgccct tcagcccccac ctt 343

```

<210> 119

<211> 4530

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral
 oncogene homolog 2 (neuro/glioblastoma derived
 oncogene homolog) (ERBB2) gene.

<400> 119

```

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ccctttcctt ccagatcctg ggtactgaaa gccttaggga agctggcctg agaggggaag 4260
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tgcttttctg ttttagttttt actttttttt ttttgtttt ttaaagacga aataaagacc 4440
caggggagaa tgggtgttgt atggggaggc aagtgtgggg ggtccttctc cacaccact 4500
ttgtccattt gcaaatatat ttggaaaa c 4530

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<210> 120

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. mouse double minute 2,
human homolog of; p53-binding protein (MDM2) gene.

<400> 120

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nacttatttc ccctagttga cctgtctata agagaattat atattttctaa ctatataacc 60
ctaggaattt agacaacctg aaattttatt acatatatca aagtggagaaa atgcctcaat 120
tcacatagat ttctttctct tagtataatt gacctacttt ggtagtggga a tagtgaata 180
cttactataa tttgacttga atatgtaggc tcatccttta caccaactcc taatttttaa 240
taattttctac tctgtcttaa atgaggagggt acttgggnnt ttttttttct taaatatggt 300
atatggacat ttaaattggt 319

```

<210> 121

<211> 2372

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;
p53-binding protein (MDM2) gene.

<400> 121

```
gcaccgcgcg agcttggtcg cttct ggggc ctgtgtggcc ctgtgtgtcg gaaagatgga 60
gcaagaagcc gagcccgagg ggcggccgcg acccctctga ccgagatcct gctgctttcg 120
cagccaggag caccgtccct ccccgatta gtgcgtacga gcgcccagtg ccctggcccg 180
gagagtggaa tgatccccga ggcccagggc gtcgtgcttc cgcagtagtc agtccccgtg 240
aaggaaactg gggagtcttg agggaccccc gactccaagc gcgaaaaccc cggatgggtg 300
ggagcaggca aatgtgcaat accaacaatgt ctgtacctac tgatgggtgct gtaaccacct 360
cacagattcc agcttcggaa caagagaccc tggtttagacc aaagccattg cttttgaagt 420
tattaaagtc tgttgggtgca caaaaagaca cttatactat gaaaga gggt ctttttttatc 480
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gttcaaata tcttctagga gatttgtttg gcgtgccaag cttctctgtg aaagagcaca 600
ggaaaatata taccatgata tacaggaact tggtagtagt caatcagcag gaatcatcgg 660
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ctacctcatc tagaaggaga gcaattagt agacagaaga aaattcagat gaattatctg 840
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catcaacttc tagtagcatt atttatagca gccagaaga tgtgaaagag tttgaa aggg 1560
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atcttatggc ctgctttaca tgtgcaaaga agctaaagaa aaggaataag ccctgcccag 1740
tatgtagaca accaattcaa atgattgtgc taacttattt cccctagttg acctgtctat 1800
aagagaatta tatatttcta actatataac cctaggaatt tagacaacct gaaatttatt 1860
cacatatatc aaagtgagaa aatgcctcaa ttcacataga tttcttctct ttagtataat 1920
tgacctactt tggtagtgga atagtgaata cttactataa tttgacttga atatgtagct 1980
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ttggtttttt ttttcttaaa tatgtatatg acatttaaat gtaacttatt attttttttg 2100
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tacagtcata tgccaccaca cctggcta at ttttgtact tttagtagag acagggtttc 2280
accgtgttag ccaggatggc ctcgatctcc tgacctcgtg atccgcccac ctcggcctcc 2340
caaagtgctg ggattacagg catgagccac cg 2372
```

<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 122
atgcttataa tattattcca acagactgta tta aaggcag tgatcactaa cacagancac 60
gacagggcga ngaggcagcc nggccgataa ncaggacgtg gccnntcggc caggggttcgc 120
tgacatgcac gctggtagct catacactgc taccctcagc acaggctgca ggaataggga 180
caagacagat gccgccggac tcttaggaag ctattttaata aatatcatcc aaanacaaaa 240
tgggaaaagg aaacaaggaa accctccggg gcacaaccac cttaggggcc aactggaatg 300
gtaattctag gttttatttc caacccaaaa nttgaggaga gga 343

<210> 123
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(258)
<223> 3' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 123
cgagtgaagt atgttggagg aacatgttgt gtctgccgtt tttgaatacc caggggtggga 60
gcttggccat ctgcatcccc acttcccata gcccaggcag agggac agag aaatggagtn 120
gggagcacag agcaggctcc aacaagacaa attccctgct gccaaaccac catgatccac 180
tctgactttg gncacaaact ctgctaaaaa caattctcta cgttcactgt tcccaagggg 240
canttttaaa cagtgggtg 258

<210> 124
<211> 443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(443)
<223> 5' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 124
gccagggctc agtgggcaag ggctctgtgc cgtngncctg tacgactacc atgcagccga 60
cgacacagag atctcctttg accccgagaa cctcatcacg ggcacgcagg tgatcgacga 120
aggctggttg cgtggctatg ggccggatca tntgttingca tgttccctgc caactacgtg 180
gagctcattg agtgaggctg agggcacatc ttgcccttcc cctctcagac atggcttc ct 240
tattgctgga agaggaggcc tggggagtgc acattcagca ctcttcagg gaataggga 300
ccccagttga ggattgagge ntcagggttc cctccggntt gggcagattc agccttttca 360
ccccaaatgg cagcaattgg cntgggtgat ttcccacaaa tcnttcctgg cattcccccg 420
acctttccca gacagtttgg ttt 443

<210> 125
<211> 1331
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1331)

<223> src homology 3 domain -containing protein
hip-55 (HIP-55) gene.

<400> 125

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atggcggcga acctgagccg gaacggggcca gcgctgcaag aggcctacgt gcgggtggtc 60
accgagaagt ccccgaccga ctgggctctc ttacctatg aaggcaacag caatgacatc 120
cgcgtggctg gcacagggga gggtagcctg gaggagatgg tggaggagct caacagcggg 180
aaggtgatgt acgccttctg cagagtgaag gaccccaact ctggactgcc caaatattgtc 240
ctcatcaact ggacaggcga gggcgtgaac gatgtgcgga agggagcctg tgccagccac 300
gtcagcacca tggccagctt cctgaagggg gcccatgtga ccatcaacgc acgggcccag 360
gaggatgtgg agcctgagtg catcatggag aaggtggcca aggcctcagg tgccaactac 42 0
agctttcaca aggagagtgg ccgcttcag gacgtgggac cccaggcccc agtgggctct 480
gtgtaccaga agaccaatgc cgtgtctgag attaaaaggg ttggtaaaga cagcttcttg 540
gccaaagcag agaaggagga ggagaaccgt cggctggagg aaaagcggcg ggccgaggag 600
gcacagcggc agctggagca ggagcgcggg gagcgtgagc tgcgtagggc tgcacgccgg 660
gagcagcgtc atcaggagca gggtagcgag gccagcccc agaggacgtg ggagcagcag 720
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ttcaagcaga aggagagggc catgtccacc acctccatct ccagtcctca gcctggcaag 840
ctgaggagcc ccttctctgc a gaagcagctc acccaaccag agaccactt tggcagagag 900
ccagctgctg ccatctcaag gccagggca gatctccctg ctgaggagcc ggcgcccagc 960
actcctccat gtctggtgca ggcagaagag gaggctgtgt atgaggaacc tccagagcag 1020
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gaccaccaca ttcagggcca ggggctcagt gggcaagggc tctgtgccc tgccctgtac 1140
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atcgaggtga tcgacgaagg ctggtggcgt ggctatgggc cggatggcca ttttggcatg 1260
ttccctgcc aactacgtgga gtcatttag tgag gctgag ggcggccgct agactagtct 1320
agagaaaaaa c 1331
```

<210> 126

<211> 430

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 126

```
gtatttccat gtcagctggg gctctcagcc gcccagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag cccaatccc aaccacacct ccaggccaat acatgcccct 120
gggactggct cagtcccagc accaccctgc aggcctcaac aaggtgggtt ttgtcccctc 180
tactccttc cagctcatcc tcaggcctct agcggcctca tcctcaacgg gcccgggaca 240
ctgaacaggt agggtaggca gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcagggcagg ttttncaagg gaggncccc gaggacggcc ttgggtnttg g ggtaagggc 360
ttaanccagt cngggctttg gtaagggccc ggnaagggat tccntgggna aattaaagg 420
aanccccagg 430
```

<210> 127

<211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(339)
 <223> 5' terminal sequence. cathepsin d (lysosomal aspartyl protease) (CTSD) gene.

<400> 127
 gtggatgagg tgcgcgactg cagaaggcca tcggggcgtn gccgctgatt cagggcgagt 60
 acatgatccc ctgtgagaag gtgtccacc c tgcccgcgat cacactgaag ctgggaggca 120
 aaggctacaa gctgtcccca gaggactaca cgctcaagggt gtcgcaggcc gggaagaccc 180
 tctgcctgag cggcttcatg ggcatggaca tcccgccacc cagcggnoac tctggatcct 240
 ggggcgacgt cttcattcgg ccgttantac attgtgtttt gaccgtgaca acaacagggt 300
 tgggtttcgc gaggcttgcc cgcttttagt ttcccaagg 339

<210> 128
 <211> 1988
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1988)
 <223> cathepsin d (lysosomal aspartyl protease) (CTSD) gene.

<400> 128
 ccatgcagcc ctccagcctt ctgccgctcg cctcttgcct gctggctgca cccgcctccg 60
 cgctcgtcag gatcccgtcg cacaagttca cgtccatccg ccggaccatg tcggagggtg 120
 ggggctctgt ggaggacctg attgccaaag gcccgcgtct aaagtactcc caggcgggtg 180
 cagccgtgac cgagggggccc attcccagagg tgctcaagaa ctacatggac gccagtgact 240
 acggggagat tggcatcggg acgccccccc agtgcttcac agtcgtcttc gacacgggct 300
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 accacaagta caacagcgac aagtccagca cctaogttaa gaatgggtacc tcgtttgaca 420
 tccactatgg ctcgggcagc ctctccgggt acctgagoca ggacactgtg tcggtgccct 480
 gccagtcagc gtcgtcagcc tctgccctgg gcggtgtcaa agtggagagg caggtctttg 540
 gggaggccac caagcagcca ggcacacact tcacgcagc caagttcgat ggcacccctg 600
 gcatggccta ccccgcatc tccgtcaaca acgtgctgcc cgtcttcgac aacctgatgc 660
 agcagaagct ggtggaccag aacatcttct ccttctacct gagcagggac ccagatgcgc 720
 agcctggggg tgagctgatg ctgggtggga cagactocaa gtattacaag ggttctctgt 780
 cctacctgaa tgtcacccgc aaggcctact ggcaggtoaa cctggaccag gtggagggtg 840
 ccagcgggct gacctgtgc aaggagggt gtgaggccat tgtggacaca ggcacttccc 900
 tcatggtggg cccggtggat gaggtgcgag agctgcagaa ggccatcggg gccgtgccgc 960
 tgattcaggg cgagtacatg atcccctgtg agaaggtgtc caccctgccc gcgatcacac 1020
 tgaagctggg aggcaaaggc tacaagctgt cccagag ga ctacacgctc aaggtgtcgc 1080
 aggcggggaa gacctctgc ctgagcgggt tcacgggcat ggacatcccg ccacccagcg 1140
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 acaacaacag ggtgggcttc gccgaggctg cccgcctcta gttcccaagg cgtccgcgcg 1260
 ccagcacaga aa cagaggag agtcccagag caggaggccc ctggcccagc ggccccctcc 1320
 acacacaccc acacactcgc ccgcccactg tcctgggcgc cctggaagcc ggccggccaa 1380
 gcccgacttg ctgttttgtt ctgtgggttt cccctccctg gggttcagaa tgctgcctgc 1440

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ctgtctgtct ctccatctgt ttggtggggg tagagctgat ccagagcaca g atctgtttc 1500
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ttgttggagc ctgcagggtg gtgctgggac tgagccagtc ccaggggcat gtattggcct 1860
ggagggtggg ttgggattgg gggctgggtgc cagccttccct ctgcagctga cctctgttgt 1920
cctccccttg ggcggctgag agccccagct gacatggaaa tacagttgtt ggctccggc 1980
ctcccctc 1988

```

<210> 129

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 5' terminal sequence. insulin -like growth factor 1 receptor (IGF1R) gene.

<400> 129

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gtggcggcac tcattgttct cgggtgcacgc ccgcttccca cacgtgcttg tggcacattt 60
tctggcagcg gtttgtggtc cagcagcggg agttgtactc at tgttgatg gtggctcttct 120
cacacatcgg cttctcctcc atggctccctg gacacaggtc ccacattcc tttgggggct 180
tattccccac aatgtagtta ttggacaccg catccaggat cagggaccag tccacagtng 240
agaggtaaca gaggtcagca tttttctcaa tcctgatggc ccccgagta atgttctca 300
ggttgtaaag cccaatatcc ttgaggatgg gtcaatcttc gaaggatgaa ccaggggcnt 360
aggttnttg gaaggagntt ttcca 385

```

<210> 130

<211> 4989

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4989)

<223> insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 130

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tttttttttt ttttgagaaa gggaatttca tcccaaataa aaggaatgaa gtctggctcc 60
ggaggagggt ccccgacctc gctgtggggg ctctgtttc tctccgccgc gctctcgctc 120
tggccgacga gtgga gaaat ctgcgggcca ggcacgaca tccgcaacga ctatcagcag 180
ctgaagcgcc tggagaactg cacggtgatc gagggctacc tccacatcct gctcatctcc 240
aaggccgagg actaccgcag ctaccgcttc cccaagctca cggtcattac cgagtacttg 300
ctgctgttcc gagtggctgg cctcgagagc ctcgagagacc tcttccccaa cctcacg gtc 360
atccgcggct ggaaactctt ctacaactac gccctggta tcttcgagat gaccaatctc 420
aagatatgg ggctttacaa cctgaggaac attactcggg gggccatcag gattgagaaa 480
aatgctgacc tctgttacct ctccactgtg gactcgtccc tgatcctgga tgcggtgtcc 540
aataactaca ttgtggggaa taagccccca aagga atgtg gggacctgtg tccagggacc 600

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atggaggaga	agccgatgtg	tgagaagacc	accatcaaca	atgagtacaa	ctaccgctgc	660
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gagaacaatg	agtgtgcca	ccccgagtg	ctgggcagct	gcagcgcgcc	tgacaacgac	780
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87/292

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<210> 131

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> 5' terminal sequence. insulin receptor
(INSR) gene.

<400> 131

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<210> 132

<211> 4691

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4691)

<223> insulin receptor (INSR) gene.

<400> 132

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89/292

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<210> 133
 <211> 451
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(451)
 <223> 5' terminal sequence. forkhead box ola
 (rhabdomyosarcoma) (FOXO1A) gene.

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<210> 134
 <211> 5723
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5723)
 <223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)
 gene.

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<400> 134
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<210> 135

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 3' terminal sequence. epidermal growth
factor receptor (avian erythroblasti c leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 135

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gccatttggc tttggcttcc ttgggaaaga agtcctgctg gtagtcaggg ttttccaggg 420
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<210> 136

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth
factor receptor (avian erythroblastic leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

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<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian
erythroblastic leukemia viral (v-erb-b) oncogene
homolog) (EGFR) gene.

<400> 137

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<210> 138
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(378)
 <223> 3' terminal sequence. tek tyrosine kinase,
 endothelial (venous malformations, multiple
 cutaneous and mucosal) (TEK) gene.

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acccaggnc cggagtgg 378

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<210> 139
 <211> 447
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(447)
 <223> 5' terminal sequence. tek tyrosine kinase,
 endothelial (venous malformations, multiple
 cutaneous and mucosal) (TEK) gene.

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<400> 139
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<210> 140

<211> 4138
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
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<222> (1)..(4138)
<223> tek tyrosine kinase, endothelial (venous
malformations, multiple cutaneous and mucosal)
(TEK) gene.

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agatcctaca atttatccag tgcttgactg gaatgacatc aaatttcaag atgtgattgg 2640
ggagggcaat tttggccaag ttcttaaggc gcgcatacag aaggatgggt tacggatgga 2700
tgctgccatc aaaagaatga aagaatatgc ctccaaagat gatcacaggg actttgcagg 2760

```

agaactggaa gttcttttga aacttggaca ccatccaaac atcatcaatc tcttaggagc 2820
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catggactac ttgagccaaa aacagtttat ccacagggat ctggctgcca gaaacatttt 3060
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tgggtgacat ttgggagaca tgtgacattt atatattgaa ttaatatccc tacatgtatt 4020
gcacattgta aaaagtttta gttttgatga gttgtgagtt taccttgtat actgtaggca 4080
cactttgcac tgatatatca tgagtgaata aatgtcttgc ctactcaaaa aaaaaaaaa 4138

```

<210> 141

<211> 395

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor
receptor superfamily, member 6 (TNFRSF6) gene.

<400> 141

```

taattccaaa cacaaggggc aaaaaaatcc tccataaatg gaagttcttt aggtggttcc 60
aggnatctgc ttcagtttat aa ctatcttc acagtttaca ttacagaaa tataaatatt 120
atttcttaaa attcacattt aatacaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaattctta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
tgatgatttt accattgcta tgtataagct gccatttgta ggcagggttt acatggggac 300
attattgaac attttcgggg ggtgggggga aaaataagg n atctatttta tccatctttg 360
gattggcaaa cctgggggttc angacatgtt caca 395

```

<210> 142

<211> 461

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(461)

<223> 5' terminal sequence. tumor necrosis factor

receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

```
tcgtaattgg catcaacttc atggaaagaa agaagcgtat gacacattga ttaaagatct 60
caaaaaagcc aatcttttga ctcttgcag a gaaaattcag actatcatcc tcaaggacat 120
tactagtgcac tcagaaaatt caaacttcag aaatgaaatc caaagcttgg tctagagtga 180
aaaacaacaa attcagttct gagtatatgc aattagtgtt tgaaaagatt cttaatagct 240
ggctgtaaat actgcttggg tttttactgg gtacatttta tcatttatta gcgctgaaga 300
gccaacatat ttgtaggttt ttaatatctc catggattct gcctccaagg gtgtttaaaa 360
tctagttggg ggaaacaaac ttccttcaag gggttaaagc ngtggcctgg ctaagtaccc 420
ccattaggga gtgtttgccg ggggttgnaa ggtttaggtt t 461
```

<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,
member 6 (TNFRSF6) gene.

<400> 143

```
gcaagagtga cacacaggtg ttcaaagacg cttctgggga gtgagggaa g cggtttacga 60
gtgacttggc tggagcctca ggggcgggca ctggcacgga acacaccctg aggccagccc 120
tggctgcccc ggccggagctg cctcttctcc cgccgggttg tggaccgct cagtacggag 180
ttggggaagc tctttcactt cggaggattg ctcaacaacc atgctgggca tctggaccct 240
cctacctctg gttcttacgt ctgttgct ag attatcgtcc aaaagtgtta atgcccaagt 300
gactgacatc aactccaagg gattggaatt gaggaagact gttactacag ttgagactca 360
gaacttggaa ggccctgcac atgatggcca attctgccat aagccctgtc ctccagggtga 420
aaggaaagct agggactgca cagtcaatgg ggatgaacca gactgcgtgc cctgccaaaga 480
agggaaaggag tacacagaca aagcccatct tctctccaaa tgcagaagat gtagattgtg 540
tgatgaagga catggccttag aagtggaaat aaactgcacc cggaccacaga ataccaagtg 600
cagatgtaaa ccaaactttt tttgtaactc tactgtatgt gaacactgtg acccttgcac 660
caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacac ca agtgcaaaga 720
ggaaggatcc agatctaact tgggggtggc ttgtcttctt cttttgcaa ttccactaat 780
tgtttgggtg aagagaaagg aagtacagaa aacatgcaga aagcacagaa aggaaaacca 840
aggttctcat gaatctccaa ccttaaatcc tgaacacagt gcaataaatt tatctgatgt 900
tgacttgagt aaatatatca ccacta ttgc tggagtcatg acactaagtc aagttaaagg 960
ctttgttcga aagaatggtg tcaatgaagc caaaatagat gagatcaaga atgacaatgt 1020
ccaagacaca gcagaacaga aagttcaact gcttcgtaat tggcatcaac ttcattggaaa 1080
gaaagaagcg tatgacacat tgattaaaga tctcaaaaaa gccaatcttt gtactcttgc 1140
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cagaaatgaa atccaaagct tggctctagag tgaaaaacaa caaattcagt tctgagtata 1260
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gattatgctc tggcatctaa catatgattc tgtagtatga atgtaatcag tgtatgttag 1560
tacaaatgtc tatccacagg ctaacccac tctatgaatc aatagaagaa gctatgacct 1620
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tgtaaagtat atgtatttga gtgcagaatt taaataaggc tctacctcaa agac ctttgc 1800
acagtttatt ggtgtcatat tatacaatat ttcaattgtg aattcacata gaaaacatta 1860
aattataatg tttgactatt atatatgtgt atgcatttta ctggctcaaa actacctact 1920
tctttctcag gcatcaaaag cattttgagc aggagagtat tactagagct ttgccacctc 1980
```

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tccatttttg ccttgggtgct catcttaat g gcctaattgca cccccaaca tggaatatc 2040
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tttggagata ctaactgctc tcagagaaag tagctttgtg acatgtcatg aacccatgtt 2160
tgcaatcaaa gatgataaaa tagattctta tttttcccc acccccgaaa atgttcaata 2220
atgtcccatg taaaacctgc taaaaatggc agcttatata tagcaatggt aaaatcatca 2280
tctggattta ggaattgctc ttgtcatacc cccaagtttc taagatttaa gattctcctt 2340
actactatcc tacgtttaaa tatctttgaa agtttgtatt aaatgtgaat tttaagaaat 2400
aatatttata tttctgtaaa tgtaaactgt gaagatagtt at aaactgaa gcagatacct 2460
ggaaccacct aaagaacttc catttatgga ggattttttt gcccttgtg tttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

<210> 144

<211> 434

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(434)

<223> 3' terminal sequence. cyclin-dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 144

```

aaagtcacta agaatcattt attnagcacc tgctgtatat tcagcattgt gggaggagct 60
gtgaaagaca cagaacagta caggggtgtg tccctgccct cgagaggttt acagtctagg 120
tgagaaaacg ggaaccagga cacatgggga gccgagagaa aacagtcacg gccagtatgt 180
tacaggagct ggaaggtntt tggggtcaga cccaataact ccaagtacac taagcacttc 240
agtccttcca ggggctcaac gttagtgcga ggaaagacaa ctactcccag ccccatatga 300
gccacgtggt catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
ttgttcgct ggctaattca aagtgcaatg aactggggag ggatgggggtg gatgaggaag 420
gttcgntgga cggt 434

```

<210> 145

<211> 257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(257)

<223> 5' terminal sequence. cyclin-dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 145

```

cttgtgtgct ntnccagggg gcaggctgaa ggggtccccag gtggacctgg agactctcag 60
ggtcgaaaac ggccgcagac cagcatgaca gatttctacc actccaaacg ccggctgac 120
ttctccaaga ggaagcccta atccgcccac aggaagcctg cagtcttgga agcgcgaggg 180
cctcaaaggc cntnctnaca tcttctgcct tagtctcagt ttgtgtgtct taattattat 240
ttgtgtttta aattttt 257

```

<210> 146

<211> 2121

99/292

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 146

```
gccgaagtca gttccttgtg gagccggagc tgggcgcgga ttgcgcgagg caccgaggca 60
ctcagaggag ggcgccatgtc agaaccggct ggggatgtcc gtcagaaccc atgcggcagc 120
aaggcctgcc gccgcctctt cggcccagtg gacagcgagc agctg agccg cgactgtgat 180
gcgctaattg cgggctgcat ccaggaggcc cgtgagcgat ggaacttcga ctttgtcacc 240
gagacaccac tggagggtga cttcgccctg gagcgtgtgc ggggccttgg cctgcccagg 300
ctctaccttc ccacggggcc ccggcgaggc cgggatgagt tgggaggagg caggcggcct 360
ggcacctcac ctgctctgct gca ggggaca gcagaggaag accatgtgga cctgtcactg 420
tcttgtaccc ttgtgcctcg ctcaggggag caggctgaag ggtccccagg tggacctgga 480
gactctcagg gtcgaaaacg gcggcagacc agcatgacag atttctacca ctccaaacgc 540
cggctgatct tctccaagag gaagccctaa tccgcccaca ggaagcctgc agtcctggaa 600
gcgcgagggc ctcaaaggcc cgctctacat cttctgcctt agtctcagtt tgtgtgtctt 660
aattattatt tgtgttttaa tttaaacacc tcctcatgta cataccctgg ccgccccctg 720
ccccccagcc tctggcatta gaattattta aacaaaaact aggcggttga atgagaggtt 780
cctaagagtg ctgggcattt ttatttttat aaatactatt taa agcctcc tcatcccgtg 840
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tccccacttg tccgctgggt ggtaccctct ggagggtgt ggtccttcc catcgctgtc 960
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ggcaggggga aggtggggtg ctggagcaga ccaccccgcc tgccctcatg gccctctga 1260
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gggcacccta gttctacctc aggcagctca agcagcgacc gccccctct ctagctgtgg 1560
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gtatatgatg ggggagtaga tctttctagg agggagacac tggccccca aatcgtccag 1680
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cacctagact gtaaacctct cgagggcagg gaccacaccc tgtactgttc tgtgtctttc 2040
acagctcctc ccacaatgct gaatatacag cagggtgctca ataatgatt cttagtgtgact 2100
ttaaaaaaaaa aaaaaaaaaa a 2121
```

<210> 147

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)
<223> 3' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 147
gatttgctaa ttgcttttatt cagaagagac cccccggagt acagcttctt tgggtaagca 60
cggagttagag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcattctgg 120
gtgggtatag aagggtcctt gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaact tgggttagggg agggagggag ggtatgagag agggaaattc agcactgggt 240
ggaaggtttc cagggaagag gggactcagc aacgaggggt gctccctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tegtcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttca c acagttgact tctgcaggag tcccnttttt gcacagggtg 420
attctgctcc ccgaagttac taaacttttt tt 452

<210> 148
<211> 379
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(379)
<223> 5' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 148
tggagtcctc tgagagagcc accaaggagg agcaggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactctta 120
ccatgaagac cctcctactg ttggcagtga tcatgatctt tggcctactg caggcccatg 180
ggaatttggt gaatttccac agaatgatca agttgacgac aggaaaggaa gccgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgacag aggatccccc aaggatgcaa 300
cggattcgct gctgtg tcac tcatgactgt ttgctacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379

<210> 149
<211> 854
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(854)
<223> phospholipase a2, group iia (platelets,
synovial fluid) (PLA2G2A) gene.

<400> 149
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca cccagcagag gagctaggcc agtccatctg catttgtc ac 120
ccaagaactc ttaccatgaa gaccctccta ctggtggcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300

```
cccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccaa atttctgagc tacaagttta gcaactcggg gagcagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgctgcc 480
acctgttttg ctagaacaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggagcacccc tegtgtgtga gtccctctt cctggaaac cttccaccca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc cttggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag cccttctata cccacccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaaagga attc 854
```

<210> 150

<211> 224

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(224)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 150

```
ggttgagcac aggnacttt attgatggna catgacaagg tgcggctccc taggcccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggagggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagttag ggtctctctc ttcctcttnt gctcttntctg 180
gggntggtgg nccagggn tn ttactccttg gaggccatnt gggc 224
```

<210> 151

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 151

```
gcgctgagta cgtcgtggag tccactggcg tcttcaccac catggagaag gctggggctc 60
atttgcaggg gggagccaaa agggctcatca tctctgcccc ctctgctgat gcccccatgt 120
tcgtcatggg tgtgaacat gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gcacccctgg gccaaaggta tccatgacaa ctttggtatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctncggga aactgtgggc gtgatggccg cggggttctt tcagaacatc atccctgcc 359
```

<210> 152

<211> 1283

<212> DNA/RNA

102/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase
(GAPD) gene.

<400> 152

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ctctctgctc ctcctgttcg acagtcagcc gcattcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaaggtgaag gtcggagtca acggatttgg tcgtattggg 120
cgctgggtca ccagggtctgc ttttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catggtttac atgttccaat atgattccac ccatggcaaa 240
ttccatggca ccgtcaaggc tgagaacggg aagcttgtca tcaatggaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtacgtc 360
gtggagtcca ctggcgtctt caccaccatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgccccctct gctgatgcc ccatgttcgt catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctcctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaactttg gtatcgtgga agga ctcattg 600
accacagtcc atgccatcac tgccaccag aagactgtgg atggcccctc cgggaaactg 660
tgcggtgatg gccgcggggc tctccagaac atcatccctg cctctactgg cgctgccaa 720
gctgtgggca aggtcatccc tgagctgaac ggggaagctca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
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tacactgagc accaggtggt ctctcttgac ttcaacagcg acaccactc ctccacctt 960
gacgtgggg ctggcattgc cctcaacgac cactttgtca agctcatttc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtggtg gacctcatgg ccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtcccc accacactga atctcccctc ctcacagtgt 1200
ccatgtagac cccttgaaga ggggaggggc ctaggagacc gcaccttgt c atgtaccatc 1260
aataaagtac cctgtgctca acc                                     1283
```

<210> 153

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 3' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 153

```
tacttaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaataa 60
aactctttag agactaagtg cgtgtttctt ttccacagta cgggtgcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gggggcttga gta ccaggcg gcggggccag 180
ctccctant ncgccccctc ttccctctcc tgttaaatac acaaatatat tataattcaat 240
ntgaatcng tctntttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttnttaaa cgttcggang ttggaaggnc tttggggcnc aggggtaggg anggcccgag 360
t                                     361
```

<210> 154

<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 5' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 154
agcgcatcaa agtngagcgc angccttgcg gaaccggctn gcggccacca agtgccggaa 60
gcggaantgg gagcgcatcg ggcttgggag gacaagggtga agacgctcaa ggccgagaac 120
gcgggngtgt cgagtaccgc cggcttcctc cgggagcagg tggcccagct caaacagaag 180
gtcatgaccc acgtnagc aa cgctnntnag ctgctgcttn gggtaaggag acacgccttc 240
tggaacgttc cctgcccctt tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300
tttcccactn gggttcacag gtagcaggcg gtggggnacc cacctggggg acntaggggg 360
cgnccgcaaa ccacattngg atttcgggcc ttcttaacct t 401

<210> 155
<211> 1797
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1797)
<223> jun b proto -oncogene (JUNB) gene.

<400> 155
ccagcagggg gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60
cgacgggggc tcgggaagcc tgacagggtt tttgcgaca gctgccggct ggctgctacc 120
cgcccgcgcc agccccgag aacgcgcgac caggcaccca gtccgggtcac cgcagcggag 180
agctcgccgc tcgctgcagc gaggccccga ggggccccgc agggaccctc ccagaccgc 240
ctgggcccgc cggatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300
agctacggga tacggccggg cccctgggtg cctctctcta cactactaca aactcctgaa 360
accgagcctg gcggtcaacc tggcgcagcc ctaccggagt ctcaaagcgc ctgggggctcg 420
cggacccggc ccagagggcg gcggtggcgg cagctacttt tctggtcagg gctcg gacac 480
cggcgcgctc ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540
cggcgtgatc acgacgacgc ctacaccccc gggacagtac ttttaccctc gcgggggttg 600
cagcgggtga ggtgcagggg gcgcaggggg cggcgctacc gaggagcagg agggcttcgc 660
cgacggcttt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720
cgtgtccctg ggcgctaccg gggggccccg ggctgggccc gggggcgtct acgcccggcc 780
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840
aggcgccggg gctgcgctcg ggaccgggag ctctgtaaccg acgaccacca tcagctacct 900
cccacacgcg cgcgcccttc cgggtggcca cccggcgcgag ctgggcttgg gccgcggcgc 960
ctccaccttc aaggaggaac cgcagaccgt gccggaggcg cgcagccggg acgccacgcc 1020
gccggtgtcc cccatcaaca tggaagacca agagcgcac aaagtggagc gcaagcggct 1080
gcggaaccgg ctggcgcca ccaagtgcg gaagcgggag ctggagcgca t cgcgcgcct 1140
ggaggacaag gtgaagacgc tcaaggccga gaacgcgggg ctgtcgagta ccgccggcct 1200
ctccggggag cagggtggccc agctcaaaca gaaggtcatg acccacgtca gcaacggctg 1260
tcagctgctg cttgggggtca agggacacgc cttctgaacg tcccctgccc ctttacggac 1320
acccctcgcg ttggacggct gggcac acgc ctcccactgg ggtccagggg gcaggcgggtg 1380
ggcaccaccc ctgggaccta ggggcgcgcg aaaccacact ggactccggc cccctaccc 1440

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```

tgcgcccagt ccttccacct cgacgtttac aagccccccc ttccactttt ttttgtatgt 1500
tttttttctg ctggaaacag actcgattca tattgaatat aatataattg tgtatttaac 1560
agggagggga agagggggcg atcgcgggcg agctggcccc gccgcctggg actcaagccc 1620
gcggggacat tgggaagggg acccccgcgc cctgccctcc cctctctgca ccgtactgtg 1680
gaaaagaaac acgcacttag tctctaaaga gtttatttta agacgtgttt gtgtttgtgt 1740
gtgtttgttc tttttattga atctatttaa gtaaaaaaaaa aattggttct ttattaa 1797

```

<210> 156

<211> 335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(335)

<223> 3' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 156

```

aagcatttta ataaaattaa caaataaata ttctaaactg tataggctac agggacaaaag 60
ggtagaagct agagggccag tctttcctgc tcaggccctc aagtcccctt tagagagacc 120
ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaaccg 180
aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240
ggtcaaagaa agcaagaccc tgcaagaggg atcccagtga ccccagaag tgactggggg 300
aaggggagcg ctatcctagg anggtggggg tgggt 335

```

<210> 157

<211> 481

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(481)

<223> 5' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 157

```

gcctggactt gtcttgggtt ccagaacctg acgaccggcg gacgcgacgt ctct tttgac 60
taaaagacag tgtccagtgc tccagcctag gagtctacgg ggaccgcctc ccgcgccgcc 120
accatgcccc acttctctgg caactggaaa atcatccgat cggaaaactt cgaggaattg 180
ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240
ccagcagtn g atcaaaaca ggaggagag act ttctaca tcaaaacctc caccaccgtg 300
cggcaccaca gagattaact tcaagggtng ggaggagttt gagggagcag antgtgggtg 360
gggagggcct gttaaggagc ngggtgaaat ggggagagtg aggattaaat ggtcttttga 420
gcagaagttc ctgaaggng aggggcccc agacntcttg gaccngagaa tttntccacg 480
t 481

```

<210> 158

<211> 969

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(969)

<223> cellular retinoic acid-binding protein 2
(CRABP2) gene.

<400> 158

```
agctttgggg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acggggaccg 120
cctcccgcg cgcaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaag 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaagg tggggaggag tttagaggagc 360
agactgtgga tgggaggccc tgtaagagcc tgggtgaaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctcctg aaggagaggg gcccgaagac ctctgtggacc agagaactga 480
ccaacgatgg ggaactgatc ctgaccatga cggcggatga cgttgtgtgc accagggtct 540
acgtccgaga gtgagtggcc acaggtagaa cgcgcggcca agcccaccac tggccatgct 600
caccgccttg cttcactgcc ccct cgtcc caccctcc ttctaggata gcgctccct 660
taccacagtc acttctgggg gtcactggga tgctcttgcc agggctcttg tttctttgac 720
ctctctctc ctccctaca ccaacaaaga ggaatggctg caagagccca gatcacccat 780
tccgggttca ctcccgcct cccaagtca gcagtcctag ccccaaacca gccagagca 840
gggtctctct aaaggggact tgagggctg agcaggaaag actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa
```

<210> 159

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 159

```
cgcggttgga ggggaggtgg ccccgntcc gccgangaan tcgccccg cc acccgagag 60
cncncagagg gaccattgac cttgggctcc ccaggaaag gccttctgat gctgctgat 120
gccttggtga ccaggagga ccctgtgaag cgtctcggg gcccgctggg gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccgggggg cctgggtgca cagtagtgct 240
tggtgctggg aggggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
aggagntct tgcagggggg gcgccccacc gatttcgttc aacc 344
```

<210> 160

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 160
gtcagtctcc cggaaccagg actgttcac cctcgaggag aagatcttga cggccacact 60
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccccc acactccacc 120
aaggcaacct gccgtngcca ctgtcctctg caccaggga ggggagccct gagccactcc 180
ctgtgggtgg cagtcactgt ccaggagggt cccccaacat gctgttcgcc ctgcttcaga 240
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc cacgttgctt 300
tttccttgcc tncgttcggg acatggccac agggccagg ggacaaccag g gggccacca 360
gggggnccag gcaanggcca agncacgggg ggcccagggt ttnaaggggc cagttt 416

<210> 161
<211> 1970
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1970)
<223> activin a receptor type ii-like 1 (ACVRL1)
gene.

<400> 161
aggaacgggt ttattaggag ggagtgggtg agctgggcca ggcaggaaga cgctggaata 60
agaaacattt ttgtccagc ccccatccca gtcccgggag gctgcgcgc cagctgcgc 120
gagcgagccc ctcccgggt ccagcccgggt ccggggccgc gccggaccc c agcccgggt 180
ccagcgctgg cgggtgcaact gcggccgcgc ggtggagggg aggtggcccc ggtccgcca 240
aggctagcgc cccgccacce gcagagcggg ccagaggga ccatgacctt gggctcccc 300
aggaaggcc ttctgatgt gctgatggcc ttggtgacct agggagacct tgtgaagcg 360
tctcggggcc cgtggtgac ctgcacg tgt gagagccac attgcaaggg gcctacctgc 420
cggggggcct ggtgcacagt agtctggtg cgggaggagg ggaggcaacc ccaggaacat 480
cggggctgcg ggaacttgca caggagctc tgcagggggc gccccaccga gttcgtcaac 540
cactactgct gcgacagcca cctctgcaac cacaacgtgt ccctggtgct ggaggccacc 600
caacctcctt cgagcagcc gggacagat ggccagctgg ccctgacctt gggccccgtg 660
ctggccttgc tggccctggt ggccctgggt gtcttgggct tgtggcatgt ccgacggagg 720
caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780
tctgagcagg gcgacacgat gttgggggac ctctggaca gtgactg cac cacagggagt 840
ggctcagggc tccccttcct ggtgcagagg acagtggcac ggcagggtgc cttggtggag 900
tgtgtgggaa aaggccgcta tggcgaagtg tggcggggct tgtggcacgg tgagagtgtg 960
gccgtcaaga tcttctcctc gagggatgaa cagtccctgt tccgggagac tgagatctat 1020
aacacagtat tgctcagaca cgac aacatc ctaggcttca tcgctcaga catgacctcc 1080
cgcaactcga gcacgcagct gtggctcatc acgcactacc acgagcacgg ctccctctac 1140
gactttctgc agagacagac gctggagccc catctggctc tgaggctagc tgtgtccgct 1200
gcatgcggcc tggcgcacct gcacgtggag atcttctgta cacagggcaa accagccatt 126 0
gccaccgcg acttcaagag ccgcaatgtg ctggtcaaga gcaacctgca gtgttgcatc 1320
gccgacctgg gctggtgtg gatgcactca cagggcagcg attacctgga catcggaac 1380
aaccgagag tgggcaccaa gcggtacatg gcaccgagg tgcaggacga gcagatccgc 1440
acggactgct ttgagtccta caagtggact gacatctg gg cctttggcct ggtgctgtgg 1500
gagattgccc gccggaccat cgtgaatggc atcgtggagg actatagacc acccttctat 1560
gatgtggtgc ccaatgacct cagcttttag gacatgaaga aggtggtgtg tgtggatcag 1620
cagaccccca ccatccctaa ccggctggct gcagaccgg tcctctcagg cctagctcag 1680
atgatcgagg agtgctggtg cccaaacccc tctgcccagc tcaccgcgt gcggatcaag 1740
aagacactac aaaaaattag caacagtcga gagaagccta aagtgattca atagcccagg 1800

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```
agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatggtgcc 1860
ctatctgggt agaggtagtg tgagtgtggt gtgtgctggg gatgggcagc t gcgcctgcc 1920
tgctcggccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970
```

<210> 162

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. lim domain protein
(RIL) gene.

<400> 162

```
gtgacctgc gcgggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60
cgccctcac catctcacgg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120
caggagacct gatccaggcc atcaatggtg agagcacaga gtcctatgac a cacctggang 180
cacagaaccg catcaagggc tgccacgata acctcacact gtctgtgagc aggcctgagg 240
gcaggagctg gccagtgcc cctgatgaca gcaaggctca ggcacacagg atccacatcg 300
ntcctgagat ccaggacggc agcccaacaa ccagcaggcg gccctcaggc accgggactt 360
gggccagaag atnnggcagan caagnct ggg gtttttncat atggaca 407
```

<210> 163

<211> 1130

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1130)

<223> lim domain protein (RIL) gene.

<400> 163

```
tgagagtccg gctcaggctc cggctgcggc tccagcccgc gatgcccacat tccgtgaccc 60
tgcgcgggcc ttgcacctgg ggettcgcgc tgggtgggccc ggacttcagc gcgcccctca 120
ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180
tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240
gcatcaaggc ctgccacgat cacctcacac tgtctgtgag caggcctgag ggcaggagct 300
ggcccagtgcc cctgatgac agcaaggctc aggcacacag gatccacatc gatcctgaga 360
tccaggacgg cagcccaaca accagcaggc ggccctcagg caccgggact gggccagaag 420
atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480
atggcagcag cgaggccacc ctgccagccc agatgagcac cctgcattgtg tctccacccc 540
ccagcgctga cccagcagag gcctcccgcg gagccgggag cagagtcgac ctgggctccg 600
aggtgtacag gatgctgcgg gagccggcgg agcccgtggc cgcgaggccc aagcagtcag 660
gtcctcttcc ctacttgcag ggcattgctag aggcggcgga gggcggggat tggcccgggc 720
ctggcgggccc ccggaacctc aagcccacgg ccagcaagct gggcgctccg ctgagcggcc 780
tgacggggct gcccgagtgc acgcgtgct gccacggaat cgtgggcacc atcgtcaagg 840
aacgggacaa gctctaccat cccgagtgtc tcatgtgcag tgact gcggc ctgaacctca 900
agcagcgtgg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960
gcgtgaagcc gcccgagggc tacgacgtgg tggcggtgta cccaatgcc aaggtggaac 1020
tcgtctgagc tgggacctg ctcccacccc tgcttcttaa ggtccctgct cggccgggtg 1080
```

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aaatatgttt caccctgtcc c tctaataaa gtcctctgc tcaaaaaaaaa

1130

<210> 164

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(310)

<223> 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 164

```
anattcggaa cgagggatcc ctctatgtc aacgtccaga acctagacaa ggcccgcaa 60
gcagtgggtg gtgctgggccc cccaatcct gctatcaatg gcagtgcacc ccgggacctg 120
tttgacatga agcccttcga agatgtcttt cgcgtgc ctc cacctcccca gtcggtgtcc 180
atgnctgagc agtccgagg ggagccctgg gttccatggg aagctgagcc ggccggaggc 240
tgaggcactg ctggcagctt caatggggat ttccnggtac gggagagcac gaccacacng 300
gggcaatatg                                     310
```

<210> 165

<211> 3664

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3664)

<223> shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 165

```
atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct 60
ccccaggact tctgtgactc ctggggcaca gaggtccaac cagggtgaagg gcctggggat 120
accccttgcc tggccccctt gccaaactg gcaggggggc caggctgggc agcagcccct 180
ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ct ccggaatg 240
agtctctgtc atcgctggag gaaggggctt ctgggtccac cccccggag gagctgcctt 300
cccatcagc ttcacccctg gggcccatcc tgctctctct gcctggggac gatagtccca 360
ctaccctgtg ctcttcttc ccccgatga gcaacctgag gctggccaac ccggtgagg 420
ggcgccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg 480
gggcagccat gccagagtca gggccctac ccctctcca ggacatgaac aagctgagtg 540
gaggcgccgg gcgcaggact cgggtggaag ggggccagct tgggggcgag gagtggacct 600
gccacgggag ctttgtcaat aagccacgc ggggctggct gcatcccaac gacaaagtca 660
tgggaccggg ggtttcctac ttggttcggt acatggggtg tgtggaggtc ctccagtcaa 720
tgcgtgccct ggacttcaac acccgactc aggtcaccag ggaggccatc agtctgggtg 780
gtgaggctgt gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc 840
tcagctctat cctggggagg agtaacctga aatttgctgg aatgccaatc actctcaccg 900
totccaccag cagcctcaac ctcatggccg cagactgcaa acagatcatc gcccaaccac 960
acatgcaatc tatctcattt gcatccggcg gggatccgga cacagccgag tatgtgcct 1020
atgttgccaa agaccctgtg aatcagagag cctgccacat tctggagtgt ccgaagggc 1080
ttgcccagga tgtcatcagc accattg gcc aggccttcga gttgcgcttc aaacaatacc 1140
```

```

tcaggaaccc acccaaactg gtcaccctc atgacaggat ggctggcttt gatggctcag 1200
catgggatga ggaggaggaa gagccacctg accatcagta ctataatgac ttcccgggga 1260
aggaaccccc cttggggggg gtggtagaca tgaggcttcg ggaaggagcc gctccagggg 1320
ctgctcgacc cactgcaccc aatgcccaga ccccagcca cttgggagct acattgcctg 1380
taggacagcc tgttggggga gatccagaag tccgcaaaca gatgccacct ccaccacct 1440
gtccaggcag agagcttttt gatgatccct cctatgtcaa cgtccagaac ctagacaagg 1500
cccggcaagc agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgcacccc 1560
gggacctgtt tgacatgaag cccttcgaag atgctcttcg ggtgcctcca cctccccagt 1620
cgggtgtccat ggctgagcag ctccgagggg agccctgggt ccatggggaag ctgagccggc 1680
gggaggctga ggcactgctg cagctcaatg gggacttctt ggtacgggag agcacgacca 1740
cacctggcca gtatg tgcctc actggcttgc agagtgggca gcctaagcat ttgctactgg 1800
tggacctga ggggtgtggt cggactaagg atcaccgctt tgaaagtgtc agtcacctta 1860
tcagctacca catggacaat cacttgccca tcatctctgc gggcagcgaa ctgtgtctac 1920
agcaacctgt ggagcggaaa ctgtgatctg ccctagcgct ctcttccaga agat gccctc 1980
caatcctttc caccctatct cctaactctc gggacctcgt ttgggagtggt tctgtgggct 2040
tggccttgtg tcagagctgg gactagcatg gactctgggt ttcatatcca gctgagttag 2100
agggtttagg tcaaaagcct ggggtgagaat cctgcctctc cccaaacatt aatcaccaaa 2160
gtattaatgt acagagtggc ccctcacctg ggcctttcct gtgccaacct gatgccctt 2220
cccaagaag gtgagtgtt gtcattgaaa atgtcctgtg gtgacaggcc cagtggaaac 2280
gtcacccttc tgggcaaggg ggaacaaatc acacctctgg gcttcagggt atcccagacc 2340
cctctcaaca cccgcccccc ccatgtttta actttgtgcc tttagaccatc tcttaggtct 2400
aatgatattt tatgcaaaaa gttcttggac cctgaattc ttcaatgaca gggatgcca 2460
caccttcttg gcttctggga cctgtgttct tgcctgagcag cctctccggg ttgggttggg 2520
ataacagagg caggagtggc agctgtcccc tctccctggg gatatgcaac ccttagagat 2580
tgccccagag cccactccc ggccaggcgg gagatggacc cc tcccttgc tcagtgcctc 2640
ctggccgggg cccctcacc caaggggtct gtatatacat ttcataaggc ctgccctccc 2700
atgttgcatg cctatgtact ctgcgcaaaa gtgcagccct tccctctgaa gcctctgccc 2760
tgctccctt tctgggaggg cggggtgggg gtgactgaat ttgggcctct tgtacagtta 2820
actctcccag gtggatt ttg tggaggtgag aaaaggggca ttgagactat aaagcagtag 2880
acaatcccc cataccatct gtagagttag aactgcattc ttttaaagtt ttatatgcat 2940
atatttttag gctgctagac ttactttcct attttctttt ccattgctta ttcttgagca 3000
caaatgata atcaattatt acattttata atcacctttt tgacttttcc aagccc tttt 3060
acagctcttg gcattttcct cgcctaggcc tgtgaggtaa ctgggatcgc accttttata 3120
ccagagacct gaggcagatg aaattttatt ccatctagga ctagaaaaac ttgggtctct 3180
taccgcgaga ctgagaggca gaagtacgcc cgaatgcctg tcagtttcat ggaggggaaa 3240
cgcaaaacct gcagtctctg agtaccttct acaggcccg cccagcctag gcccggggtg 3300
gccacaccac agcaagccgg cccccctct tttggccttg tggataaggg agagttgacc 3360
gttttcatcc tggcctcctt ttgctgtttg gatgtttcca cgggtctcac ttataccaaa 3420
gggaaaactc ttcattaaag tccgtatttc ttctaaaaaa aaaaaaaaaa aaatacattt 3480
atacatcacc tttttgactt ttccaagccc ttttacagct cttggcattt tcctcgccca 3540
ggcctgtgag gtaactggga tcgcaccttt tataccagag acctgaggca gatgaaattt 3600
atttccatct aggactagaa aaacttgggt ctcttaccgc gagactgaga ggcagaagtc 3660
agcc 3664

```

<210> 166

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 166

110/292

```

gagcacaggg tncctttattg atggtacatg acaagggtgcg gctccctagg cccctcccct 60
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180
tgggtggtcca ggggt cttac tcccttgagg ccatgtgggc atgagggtcca ccaccctgtt 240
gctgtagcca aattcgttgt cataccaggg aaatgagctt gacaaagtgg tcgttgaggg 300
caatgccagc cccagcnttc gaagggtggag gantgggttt cgcntttgaa gtcagaggag 360
accacctggg tgctcagttt agcccagggg tgcccttgag ggggcccctc gacgttt ttt 420
tcaccacctt tttgatntca tcatntttt

```

<210> 167

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 167

```

tgttcgacag tcagccgcat cttcttttgc gtgcgcagcc gagccacatc gctgagacac 60
catggggaag gtgaagggtcg gagtcaacgg atttggtcgt attgggcgcc tggtcaccag 120
ggctgctttt aactctggta aagtggata t tggtgccatc aatgaccctc tcattgacct 180
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaatc catgggcacc 240
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat ccatttcacc atcttcagg 300
gagcgagatc cctccaaaat tcaagtgggg ggcgatgctg ggcgcttgag ttacgttcgt 360
gggagttcca ctgggccttc tttcaaccac ccttgagaa gggtttgggg gttcattttt 420
caaggggggg gagcccaaan gggctttcat tttttggccc ccttttt

```

<210> 168

<211> 316

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(316)

<223> 3' terminal sequence. desmin (DES) gene.

<400> 168

```

ggcttgtgtt tnttntctct ttattgtttc tctccagagc cctgcagca ggggagggga 60
gggcgtgggg aggtgggcgc cctcccacc agcctgagac cgctctctgc ctctctctc 120
tctctctctc tccagcatct cac ccacttt ctctccttct naatctcctg ctcccacctc 180
cagcaccttc ggggattccc tcttgtagcc cctgctttct aagtccaccc ggggctgggg 240
aaaggaaagt aagagaccac ggggacaatt tcaagcccc cagtntccac aggggctagt 300
cccctgggnt acctgc

```

<210> 169

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 5' terminal sequence. desmin (DES) gene.

<400> 169

```
atctcccat ccagacctac tctgccctca acttccgag a aaccagccct gagcaaaggg 60
gttctgaggt ccataccaag aagacggtga tgatcaagac catcgagaca cgggatgggg 120
aggtcgctcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agaccctctg 180
ccaccagaga ccgtcctcac ccctgtcctc actgtctcct gaagccagcc ttcttccatc 240
ccagggacac cacacca gc cttcagtctt ccccttcaca gcctctggac cctcctcac 300
tgggccattc cctcgtggtt cccaacagc ggacataggc ccatccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgcggg aaccccagtt gttgaggctt tggttgtttg 420
ggcagttgag ttgaggcttt                                     440
```

<210> 170

<211> 2218

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2218)

<223> desmin (DES) gene.

<400> 170

```
cctcgccgca tccactctcc ggccggccgc ctgccgcgc cctcctcc gt gcgcccggcca 60
gcctcgcccg cgccgtcacc atgagccagg cctactcgtc cagccagcgc gtgtcctcct 120
accgcccgcac cttcgggcgc gccccgggct tcccgtcgg ctcccgcctg agctogcccg 180
tgttcccgcg ggccgggttt ggctctaagg gctcctccag ctcggtgacg tcccgcgtgt 240
accaggtgtc gcgcacgtcg ggccgggg ccg ggggcctggg gtcgctgcgg gccagccggc 300
tggggaccac ccgcacgccc tcctcctacg gcgcaggcga gctgctggac ttctcactgg 360
ccgacgcggt gaaccaggag tttctgacca cgcgcaccaa cgagaagggt gagctgcagg 420
agctcaatga ccgcttcgcc aactacatcg agaagggtgc cttcctggag cagcagaacg 480
cgctcgccgc cgaagtgaac cggctcaagg gccgcgagcc gacgcgagtg gccgagctct 540
acgaggagga gctgcgggag ctgcggcgcc aggtggagggt gctcactaac cagcgcgcgc 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca ggggtcaag gccagctgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggacg 720
tgatgcagc tactctagct cgcattgacc tggagcgcag aattgaatct ctcaacgagg 780
agatcgcggt ccttaagaaa gtgcatgaag aggagatccg tgagttgcag gctcagcttc 840
aggaacagca ggtccagggt gagatggaca tgtctaagcc agacctcact gccgccctca 900
gggataatcg ggctcagtat gagac catcg cggctaagaa catttctgaa gctgaggagt 960
ggtacaagtc gaaggtgtca gacctgacct aggcagccaa caagaacaac gacgccctgc 1020
gccaggccaa gcaggagatg atggaatacc gacaccagat ccagtcctac acctgcgaga 1080
ttgacgccct caagggcact aacgattccc tgatgaggca gatgcgggaa ttggaggacc 1140
gatttgccag tgaggccagt ggctaccagg acaacattgc gcgcctggag gaagaaatcc 1200
ggcacctcaa ggatgagatg gcccgccatc tgcgcgagta ccaggacctg ctcaacgtga 1260
agatggccct ggatgtggag attgccacct accggaagct gctggaggga gaggagagcc 1320
ggatcaatct ccccatccag acctactctg ccctcaactt ccgagaaacc agccctgagc 1380
aaaggggttc tgaggtccat accaagaaga cgggtgatgat caagaccatc gagacacggg 1440
atggggagggt cgtcagtgag gcgacacagc agcagcatga agtgctctaa agacgagaga 1500
ccctctgcc aagagaccg tcctcaccct tgtcctcaat gctccctgaa gccagccctt 1560
```

112/292

```

cttccatccc agga caccac acccagcctc agtcctcccg tcacagcctc tgacccctcc 1620
tcactggcca tccctcgtgg tccccaacag cgacatagcc catccctgcc tggtcacagg 1680
catgccccgg ccacctctgc ggaccccagc tgtgagcctt ggctgttggc agtgagtgag 1740
cctggctctt gtgctggatg gagcccaggc gggagcgggtg gccctgtccc tcc cacctct 1800
gtgacctgag gcctacgctt tggctctgga gatagcccca gagcaggggtg ttgggatact 1860
gcagggccag gactgagccc cgcagacctc cccagcccct agcccaggag agagaaagcc 1920
aggcaggtag cctgggggac tagccctgtg gagactgggg ggcttgaaat tgtccccgtg 1980
gtctcttact ttcctttccc cagcccag gg tggacttaga aagcaggggc tacaagaggg 2040
aatccccgaa ggtgctggag gtgggagcag gagattgaga aggagagaaa gtgggtgaga 2100
tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggt gggaggggag 2160
cccacctccc cagcctctcc cccccctgc tgcaggggct ctggagagaa acaataaa 2218

```

<210> 171

<211> 367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(367)

<223> 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 171

```

gatccacgcc cgctacatcc ttaccaaccg tggcatcgcc agatgttggg aaagtaccag 60
caaggagact ttgggttactg tcctcgtgtg tactgtgaga accagccaat gcttccatt 120
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgccccaa gtgcatggat 180
gtgtacacac ccaagtcatc aagacaccat cacacggatg ggcgcctac t ttcggcactg 240
gtttccctca catgctcttc atgggtgcat cccgagtacc ggccaagggt gaccttgcca 300
accagtttgt gccaggggtt ttacggtttt caaggttcca tncggtgggg cttaccaggt 360
tgcagggt

```

<210> 172

<211> 1128

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1128)

<223> casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 172

```

gcttctcgtt gtgccccgcc cgcaagcgcc ctctcoggg ccttc gtgac agccagggtcg 60
tgcgcggggtc atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120
accggggact ccgtgtcccg gcatccaccg cggcacctga cccttggcgc ttgcgtgttg 180
ccctcttccc caccctccct aatttccact cccccacc cacttgcct gccgcggtcg 240
ggtccgcggc ctgcgctgta gcgg tcgccc cggttccctg gaagtagcaa cttccctacc 300
ccaccccagt cctgggtccc gtccagccgc tgacgtgaag atgagcagct cagaggaggt 360
gtcctggatt tcctggttct gtgggtcccg tggcaatgaa ttcttctgtg aagtggatga 420
agactacatc caggacaaat ttaatcttac tggactcaat gagcaggtcc ctactatcg 480
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540

```

113/292

```

ccagagtgac ctgattgagc aggcagccga gatgctttat ggattgatcc acgcccgcta 600
catccttacc aaccgtggca tcgcccagat gttggaaaag taccagcaag gagacttttg 660
ttactgtcct cgtgtgtact gtgagaacca gccaatgctt ccca ttggcc ttccagacat 720
cccaggtgaa gccatgggtga agctctactg ccccaagtgc atggatgtgt acacacccaa 780
gtcatcaaga caccatcaca cggatggcgc ctacttcggc actggtttcc ctcacatgct 840
cttcatgggt catcccagat accggcccaa gagacctgcc aaccagtttg tgcccaggct 900
ctacggtttc aagatccatc cg atggccta ccagctgcag ctccaagccg ccagcaactt 960
caagagccca gtcaagacga ttgctgatt ccctcccca cctgtcctgc agtctttgtc 1020
ttttcctttc ttttttgcca ccctttcagg aaccctgtat ggtttttagt ttaaattaaa 1080
ggagtcgtta tcgtgggtgg aatatgaaat aaagtagaag aaaaggcc 11 28

```

<210> 173

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 3' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 173

```

gggttttttt ctnaaaaaaaa cctttgagtt gcaggtcagg tnagttgggt ctggaagtac 60
cggaagttct gttggnatga gagagacttg tctacaggca ggnaaaccca agtttgccaa 120
acaaaggcag taaccccagc gaccagctgc tgctgtgca cggtgaggag gaggaggaca 180
ccatggacac gagtggaggc tggatgggac aacgcagtgg acatctgcta atg ctctaac 240
acgggggttg ngctacttct gagaagagcg aggtnagtgg ggatnctata caagagggct 300
ntacaaactg gggcactggg atagggtagt tcctttgggn ggggtcaagg gggctctacc 360
ccgtccnttg agctctngtg tncactnccg ttgggggata ccntcccaca cattcagggc 420
cantcaggna caattttacc aggtgntccc a ctgtttcac aggggggattt aagtt 475

```

<210> 174

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 174

```

ggatcatctct tgcctgaagc tgagatatgc tgaccagcgc ctgtcttcag actgtgaaga 60
ccagatccga atcattatcc aggagtccgc cctggactac cgcctggatc ctcagctcca 120
gctgcactgc tcagacgaga tctccagtct atgtgtgtaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggc caacctgctc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaagca gacatctttg ttgacccggc 300
acttcatact tgcttgtgcc ctgggacatt aaacaccaat gcgcagcatt caccctgggc 360
cgcgggcggt caaattgttc ctgtnttcat ggggaaggac tgggagggtt aaggcgggtt 420
gaggtttaca gcccgagttg caaaaaggcg cttcattgac ccggtttgag gtgttggtt 480
ttt 483

```

<210> 175
 <211> 3909
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(3909)
 <223> golgi apparatus protein 1 (GLG1) gene.

<400> 175
 ggcacgaggc tgcgcgcgga ctcaagatgg cggcgtgtgg acgtgtacgg aggatgttcc 60
 gcttgtcggc ggcgctgcat ctgctgctgc tattcgcggc cgggggcaga aactccccgg 120
 ccaggggcgtc ccacagccag ggccagggtc cgggggccaa ctttgtgtcc ttcgtagggc 180
 aggcgggagg cggcgggccc gcggtcagc agctgcccc gctgcctcag tcatcgcagc 240
 ttcagcagca acagcagcag cagcaacagc aacagcagcc tcagccgccc cagccgcctt 300
 tcccggcggg tgggcctccg cggcggggag gagcgggggc tggggtgggc tggaag ctgg 360
 cggaggaaga gtcctgcagg gaggacgtga cccgcgtgtg ccctaagcac acctggagca 420
 acaacctggc ggtgctcgag tgcctgcagg atgtgaggga gcctgaaaaat gaaatttctt 480
 cagactgcaa tcatttgttg tggaattata agctgaacct aactacagat cccaaatttg 540
 aatctgtggc cagagagggt tgcaaatcta ctat aacaga gattaaagaa tgtgctgatg 600
 aaccggttgg aaaagggttac atggtttcct gcttagtgga tcaccgaggc aacatcactg 660
 agtatcagtg tcaccagtac attaccaaga tgacggccat catttttagt gattaccgtt 720
 taatctgtgg cttcatggat gactgcaaaa atgacatcaa cattctgaaa tgtggcagta 780
 ttcggcttgg agaaaaggat gcacattcac aaggtgaggt ggtatcatgc ttggagaaag 840
 gcctggtgaa agaagcagaa gaaagagAAC ccaagattca agtttctgaa ctctgcaaga 900
 aagccattct cgggttggct gagctgtcat cggatgactt tcacttagac cggcatttat 960
 attttgcttg ccgagatgat cgggagcgtt tttgtgaaaa tacacaagct ggtg agggca 1020
 gagtgataaa gtgcctcttt aaccataaat ttgaagaatc catgagttaa aagtgtcgag 1080
 aagcacttac aaccgcgcaa aagctgattg ccagagatta taaagtcagt tattcattgg 1140
 ccaaatcctg taaaagtgaac ttgaagaaat accggtgcaa tgtggaaaac cttccgcgat 1200
 cgcgtgaagc caggctctcc tacttggtta a tgtgcctgga gtcagctgta cacagagggc 1260
 gacaagtcag cagtgaagtgc cagggggaga tgctggatta ccgacgcag ttgatggaag 1320
 acttttctct gagccctgag atcatcctaa gctgtcgggg ggagattgaa caccattgtt 1380
 ccgattaca tcgaaaagga cggaccctac actgtctgat gaaggtagtt cgaggggaga 1440
 aggggaacct tggaatgaac tgccagcagg cgcttcaaac actgattcag gagactgacc 1500
 ctggtgcaga ttaccgcatt gatcgagctt tgaatgaagc ttgtgaatct gtaatccaga 1560
 cagcctgcaa acatataaga tctggagacc caatgactc gtctgacctg atggaacatt 1620
 tatacacaga gaagatggtg gaagactgtg aacacgctct ct tagagctg cagtatttca 1680
 tctcccgga ttggaagctg gaccctgtcc tgtaccgcaa gtgccaggga gacgcttctc 1740
 gtctttgcca caccacgggt tggaatgaga ccagtgaatt tatgcctcag ggagctgtgt 1800
 tctcttgttt atacagacac gcctaccgca ctgaagaaca gggaaggagg ctctcacggg 1860
 agtgccgagc tgaagtc caa aggatcctac accagcgtgc catggatgtc aagctggatc 1920
 ctgccctcca ggataagtgc ctgattgatc tgggaaaatg gtgcagtgaag aaaacagaga 1980
 ctggacagga gctggagtgc cttcaggacc atctggatga cttggtgggtg gagtgtagag 2040
 atatagttgg caacctcact gagttagaat cagaggatat ccaaatagaa gccttg ctga 2100
 tgagagcctg tgagcccta attcagacat tctgccacga tgcggataac cagatagact 2160
 ctggggacct gatggagtgt ctgatacaga acaaacacca gaaggacatg aacgagaagt 2220
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 agtttaaaat ggcttgcaag gaggacgtgt tgaagctttg cccaaacata aaaaagaagg 2340
 tggacgtggg gatctgcctg agcacgaccg tgcgcaatga cactctgcag gaagccaagg 2400
 agcacagggt gtccctgaag tgccgcaggc agctccgtgt ggaggagctg gagatgacgg 2460
 aggacatccg cttggagcca gatctatacg aagcctgcaa gagtgacatc aaaaacttct 2520
 gtccgctgt gcaatatggc aacgctcaga ttatcgaatg tctgaaagaa aacaagaagc 2580
 agctaagcac ccgctgccac caaaaagtat ttaagctgca ggagacagag atgatggacc 2640
 cagagctaga ctacaccctc atgagggtct gcaagcagat gataaagagg ttctgtccgg 2700

115/292

```

aagcagattc taaaaccatg ttgcagtgtc tgaagcaaaa taaa aacagt gaattgatgg 2760
atcccaaatg caaacagatg ataaccaagc gccagatcac ccagaacaca gattaccgct 2820
taaaccatgt gttaagaaaa gcctgtaaag ctgacattcc taaattctgt cacgggtatcc 2880
tgactaaggc caaggatgat tcagaattag aaggacaagt catctcttgc ctgaagctga 2940
gatatgctga ccagcgccct g tcttcagact gtgaagacca gatccgaatc attatccagg 3000
agtccgccct ggactaccgc ctggatcctc agctccagct gcactgctca gacgagatct 3060
ccagtctatg tgctgaagaa gcagcagccc aagagcagac aggtcagggtg gaggagtgcc 3120
tcaagggtcaa cctgctcaag atcaaaacag aattgtgtaa aaaggaagtg ctaaaccat gc 3180
tgaaggaaag caaagcagac atctttgttg acccggtact tcatactgct tgtgccctgg 3240
acattaaaca ccactgcgca gcactcacc ctggcgcggt gcgtcaaatg tcctgtctca 3300
tggaagcact ggaggataag cgggtgaggt tacagcccga gtgcaaaaag cgcctcaatg 3360
accggattga gatgtggagt tacgcagcaa ag gtggcccc agcagatggc ttctctgato 3420
ttgccatgca agtaatgacg tctccatcta agaactacat tctctctgtg atcagtggga 3480
gcatctgtat attgttcctg attggcctga tgtgtggacg gatcaccaag cgagtgcac 3540
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caaccccggtg ttagagcatt agcagatgtc cactgcgttg tcccatccag cctccactcg 3720
tgtccatggt gtccctcctc tcctcacctg gcagcagcag cagctgggtc ctgggggttac 3780
tgcccttgtt tggcaaactt gggtttacct gcctgtagac aagtct ctct cataccaaca 3840
gaacttcggt tacttcaga accaactcac ctgacctgca actcaaaggc ttttttaaga 3900
aaaccacca                                     3909

```

<210> 176

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. endothelin receptor
type b (EDNRB) gene.

<400> 176

```

gttaagatca aacctcacia agagaaatag aatgtttgaa aggctatccc aaaagacttt 60
tttgaatctg tcattcacat accctgtgaa gac aatacta tctacaattt tttcaggatt 120
attaaaaatc tcttctttca ctatcgtagc ttaaactctg tttgggtttg tcatctgtaa 180
atacttacct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acccatgctg tgggttaaat 360
gggtttctag gcatatgtat tatggctatt                                     390

```

<210> 177

<211> 4286

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4286)

<223> endothelin receptor type b (EDNRB) gene.

<400> 177

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 tcctgatacc ctttcttct ccatgtcagt atcatgttct ctaattatct tgccaaattt 3600
 tgaaactaca cacia aaagc atacttgcat tatttataat aaaattgcat tcagtggctt 3660

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ttctttacat actcaaaacc aagatagaaa aagggtgctat cgttcaactt caaaacatgt 3780
ttcctagtat taaggactttt aatatagcaa cagacaaaat tattgttaac atgg atgtta 3840
cagctcaaaa gatttataaa agattttaac ctattttctc ccttattatc cactgctaata 3900
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gtttatagca aaacatgggt atgctgtagc taactttata aaagtgtaat ataacaatgt 4020
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actgtacaga cactaattca ttaaatacta attgattgtt taaaagaaat ataaatgtga 4200
caagtggaca ttatttatgt taaatataca attatcaagc aagtatgaag ttattcaatt 4260
aaaatgccac atttctggtc tctggg 4286

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<210> 178

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 3' terminal sequence. granzyme b (granzyme
2, cytotoxic t-lymphocyte-associated serine
esterase 1) (GZMB) gene.

<400> 178

```

acancagaga tccatttatt acagtcctgc aaccocgact gccacccct tgggaattct 60
tgccctctgc ccagagatgg tcaggccag aggaaggta gtctcatgcc tgctgttaga 120
ggcgnntcat tgttctcttt atccagggca ggaagntga gaccttgatg tagactcctg 180
gggggtgtccc ttttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
ggggccccc ggagttcccc cttgaaacog gtctgtgtct tctttggatc cccacacaa 300
atntcagtg gctctgctgt aattgccatg ggaaggagac ggttcac ant ggcagttcc 360
ttctgcactn ttcaggaaca atttctgaa gtgtgggttg ctaaagtgt cattgagaaa 420
taaccccag ccaggccaaa ttgaaaagtt gcctgggnnt tt 462

```

<210> 179

<211> 960

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic
t-lymphocyte-associated serine esterase 1) (GZMB)
gene.

<400> 179

```

agcagctcca accagggcag ccttcctgag aagatgcaac caatcctgct tctgctggcc 60
ttcctcctgc tgcccagggc agatgcaggg gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggac agaagtctct gaagaggtgc 180
ggtggcttcc tgatacaaga cgacttctgt ctgacagctg ctactgttg ggggaagctcc 240
ataaatgtca ccttgggggc ccacaatac aaagaacagg agcc gacca gcagtttatc 300
cctgtgaaaa gacccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360

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118/292

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atgctactgc agctggagag aaaggccaag cggaccagag ctgtgcagcc cctcaggcta 420
cctagcaaca aggcccaggt gaagccaggg cagacatgca gtgtggccgg ctgggggcag 480
acggccccc tgggaaaaca ct cacacaca ctacaagagg tgaagatgac agtgcaggaa 540
gatcgaaagt gcgaatctga cttacgcat tattacgaca gtaccattga gttgtgcgtg 600
ggggaccag agattaaaaa gacttccttt aagggggact ctggaggccc tcttgttgt 660
aacaaggtgg cccagggcat tgtctcctat ggacgaaaca atggcatgcc tccacgagcc 720
tgcacaaaag tctcaagctt tgtacactgg ataaagaaaa ccatgaaacg ctactaacta 780
caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840
tacactggga gaggtgccag caactgaata aatacctctc ccagtgtaaa tctggagcca 900
agtccagatt tacactggga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

```

<210> 180

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 3' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 180

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aaaaaaataa aacagcaaaa gtagcaaaaa atatatgacc tttttaaaaa cattttcctt 120
ttttttcttt tttgttttta atatatagca actga tgcct cccagccacc agngcatct 180
taccgatgg gtaaattctt ggtaacgacc cttttaaaaa gacatgtaaa tatatactca 240
gntttataca ctttgtgttt tcttcatagc tatntacaga gccccagtt tgggctgggc 300
cagggggcan caacactgcc cccaacctgg gccttcgct caccatctc tgggtaccgg 360
gcntttgggt cag gcaaagc aaactagtnt cgggtttatt angccactgg naccaccttt 420
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```

<210> 181

<211> 463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(463)

<223> 5' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 181

```

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caggactgcc tggggggagg agtgggagcc aatgaacagg catgcaagt agagcttcct 120
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ttgctttgct gaccaaagtc ctgggtacca gaggatggtg aggcgaaggc aggttggggg 360
cagtgttggt gccngggggc agcccaaac tgggggcttc tgtatatagc tattgaagaa 420

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aacacaaaatg tattaatctg agtatatatatt ttacatgtnt ttt

463

<210> 182

<211> 4066

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4066)

<223> fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

<400> 182

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cgccggtgca gccgcagcgc gcggaggaac cggggtgtgc cgggagctgg gcggccacgt 120
ccggacggga ccgagacccc tcgtagcgca ttgcggcgac ctgcgcttcc ccggcccgca 180
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gccgcccggga gtcgagcgcc ggccgcggag ctcttgccgc cccgccagga cccgaacaga 540
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gagctcactg tggagtatcc atggagatgt ggagccttgt caccaacctc taactgcaga 720
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tgaccgcga gccggtgccc gaccttgctt gaacaagccc agccctgggg agccctgtg 840
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120/292

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<210> 183

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), catalytic subunit, alpha isoform
(PPP2CA) gene.

<400> 183

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ccccaaccac cacggctcctc tggatctgac cacagcaagt cacacattgg accctcatgg 180
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agaccacatg gtagacagaa gatctgcccc tccaccaagg cagtgagagg aagatagtca 300
aaaagatctg taaaatattt ccaaacattt ggcatttcca tattttctta aacattcatt 360
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<210> 184

<211> 2181

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

121/292

<220>
 <221> misc_feature
 <222> (1)..(2181)
 <223> protein phosphatase 2 (formerly 2a),
 catalytic subunit, alpha isoform (PPP2CA) gene.

<400> 184
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 ttggtggcaa atcaccagat acaaattact tgtttatggg agattatggt gacagaggat 480
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 atgaatgttt aagaaaatat ggaaatgcaa atgtttggaa atattttaca gatctttttg 660
 actatcttcc tctcactgcc ttggtggatg ggcagatctt ctgtctacat ggtggtctct 720
 cgccatctat agatacactg gatcatatca gagcacttga tcgcctacaa gaagttcccc 780
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 gagcaacagt aactccaaag tgtcagaaaa tagttaacat tcaaaaaact tgttttcaca 1260
 tggacaaaaa gatgtgccat ataaaaatac aaagcctctt gtcacataca gccgtgacca 1320
 ctttagaatg aaccagttca ttgcatgctg aagcgacatt gttggtcaag aaaccagttt 1380
 ctggcatagc gctatttgta gttacttttg ctttctctga gagactgcag ataataagat 1440
 gtaaacatta acacctcgtg aatacaattt aacttccatt tagctatagc tttactcagc 1500
 atgactgtag ataaggatag cagcaaaaaa tcattggagc ttaatgaaca tttttaaaaa 1560
 taattaccaa ggccctccctt ctacttgtga gttttgaaat tgttcttttt attttcaggg 1620
 ataccgttta atttaattat atgatttgct tgcactcagt ttattcccta ctcaaatctc 1680
 agcccatgtg tgttctttgt tattgtcaga acctgggtgag ttgttttgaa cagaactgtt 1740
 ttttccctt cctgt aagac gatgtgactg cacaagagca ctgcagtgtt tttcataata 1800
 aacttgtgaa ctaagaactg agaaggtcaa attttaattg tatcaatggg caagactggt 1860
 gctgtttatt aaaaaagtta aatcaattga gtaaatttta gaattttag actttaggtt 1920
 aaaataaaaa tcaagggcac tacataacct ctctggtaac tccttgacat tctt cagatt 1980
 aacttcagga tttatttgta tttcacatat tacaatttgt cacattgttg gtgtgcactt 2040
 tgtgggttct tcctgcata taacttgttt gtaagaaagg aaatctgtgc tgcttcagta 2100
 agacttaatt gtaaaaccat ataacttgag atttaagtct ttgggttggt ttttaataaa 2160
 acagcatggt ttcaggtaga g 2181

<210> 185
 <211> 375
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(375)
 <223> 5' terminal sequence. homo sapiens, clone
 image:4054156, mrna, partial cds (EST R55460)
 gene.

122/292

<400> 185

```
cgaagaggat gaggaagagc tnetgctgct gcancaagag ctccaggccg ggctgcgcac 60
caaggccctg attgtggatg agtcctgccg ggggtnacca tcttccaaca tagggatata 120
cctccctcct tcttataact gaagatcctg gagcccgga gattcag ggc agacagaccc 180
tgataatgag cctggcaggg aagggcaacc aacatcttgt aacttgcttt cccaccctg 240
tttctggggg cagagcaatt gcccaatttc taccctaata caaagtccct ggggtgtnggt 300
gggggttaaac gtgctggtgc atcctagggtc atccaagagt gaggcgccaa gttcctgagg 360
aagggggcac agaac 375
```

<210> 186

<211> 542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(542)

<223> 3' terminal sequence. immunoglobulin kappa
constant (IGKC) gene.

<400> 186

```
gcaaagattc acaatatatta ttatttctcc tccaacatta gcataattaa agccaaggag 60
gaggaggggg gtgaggtgaa agatgagctg gaggaccgca ataggggtag gtccctgtg 120
gaaaaagggt cagaggccaa aggatgggag ggggtcaggc tgganctgag gagcagggtg 180
gggcacttct ccc tctaaca ctctcccctg ttgaagctct ttgtgacggg cgagctcagg 240
ccctgatggg tgacttcgca ggcgtagact ttgtgtttct cgtagtctgc tttgctcagc 300
gtcagggtgc tgctgaggct ntaggggtgt gtccttgctg tctgtctctg tgacactctc 360
ctgggggant taccnatttt gggagggggt tatccacctt ccactgtact ttggc ctctc 420
tggggtaga agttttttca gcaggcacac aacagaggca nttccagatt tncaactgct 480
catcagatgg ccgggaagnt gaaggncagt nggtgcagcc acatttcttt tgatccncca 540
ct 542
```

<210> 187

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(296)

<223> 5' terminal sequence. melanocortin 1
receptor (alpha melanocyte stimulating hormone
receptor) (MC1R) gene.

<400> 187

```
atcacctgca gctccatgct gtccagcctc tgcttctctg gcgccatcgc gtggaccgct 60
acatctccat cttctacgca ctgnctacca cagcatcgtg accctgccgc gggcgcggaag 120
nccgttgccg ccactctggg ggccagtgtc gtcttcagca cgctcttcat cgctacttac 180
gaccacgtgg ccgtcctgct gtgcctcgtg gtcttcttcc tggctatgct ggtgctcatg 240
gccgtgctgt acgtccacat gctggcccgg gcttgccagc acgccaggg cattcg 296
```

<210> 188

123/292

<211> 1270
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1270)
<223> melanocortin 1 receptor (alpha melanocyte
stimulating hormone receptor) (MC1R) gene.

<400> 188
ggagagggtg tgagggcaga tctgggggtg cccagatgga aggaggcagg catggggggac 60
accaagggc ccctggcagc accatgaact aagcaggaca cctggagggg aagaactgtg 120
gggacctgga ggcctccaac gactccttcc tgcttcctgg acaggactat ggctgtgcag 180
ggatcccaga gaagacttct gggctccctc aactccaccc ccacagccat cccccagctg 240
gggctggctg ccaaccagac aggagcccgg tgccctggagg tgtccatctc tgacggggctc 300
ttcctcagcc tggggctggg gagcttgggtg gagaacgcgc tgggtggg ggc caccatcgcc 360
aagaaccgga acctgcactc acccatgtac tgcttcatct gctgcctggc cttgtcggac 420
ctgctggtga gcgggagcaa cgtgctggag acggcgcgtc tctcctgctt ggaggccggg 480
gcactggtgg ccggggctgc ggtgctgcag cagctggaca atgtcattga cgtgatcacc 540
tgagctcca tgctgtccag cctct gcttc ctgggcgcca tcgccgtgga ccgctacatc 600
tccatcttct acgcactgcg ctaccacagc atcgtgaccc tgccgcgggc gcggcaagcc 660
gttgcgccca tctgggtggc cagtgtcgtc ttccagcagc tcttcacgc ctactacgac 720
cacgtggccg tctgctgttg cctcgtgggc ttcttcctgg ctatgctggg gctcatggcc 780
gtgctgtacg tccacatgct ggcccgggccc tgccagcacg cccagggcac cgcccggctc 840
cacaagaggc agcgcgccgg ccaccagggc ttggccctta aaggcgtgt caccctcacc 900
atcctgctgg gcattttctt cctctgctgg ggccccttct tctgcatct cacaactcatc 960
gtcctctgcc ccgagcacc cagctgcggc tgcatcttca agaac ttcaa cctctttctc 1020
gccctcatca tctgcaatgc catcatcgac cccctcatct acgccttcca cagccaggag 1080
ctccgcagga cgctcaagga ggtgctgaca tgctcctggg gaggcgggtg cagcgccttt 1140
aagtgtgctg ggcagaggga ggtggtgata ttgtgtgggc tggttcctgt gtgaccctgg 1200
gcagttcctt acctccctgg tccccgtttg tcaaagagga tggactaaat gatctctgaa 1260
agtgttgaag 1270

<210> 189
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(336)
<223> 3' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 189
ccaanaccaa atccgagccc ttggaccaaa ctgcctgctg ccgagagccg tccgcgtaga 60
gcctccgtct ccggcgagat gtccgagcgc aaagaaggca gaggcaaagg gaagggcaag 120
aagaaggagc gaggctcgnc a agaagccgg ntccgcgggc ggngcagcag gagcccagcc 180
ttgcctcccc aattnaaaga gatgaaaagc caggaatcgg ctgcagggttc caaactagtc 240
cttcgggtgtg aaaccagttc tgaatactcc tctctcagat tcaagtgggt caagaatggg 300
gaatgaattg aatcgaaaaa nncannccac aaaatt 336

124/292

<210> 190
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(366)
 <223> 5' terminal sequence. neuregulin 1 (NRG1) gene.

```
<400> 190
tctcaacaat atgctcactg gaga tgacgt ttttagatac gtattgattc accagctgga 60
cattctcggg gggtnngtta ggatggtgag gccattggc aatgttcac atattgtttc 120
gttcagaccg aagctctgcc agagacggtc atgcagcttt ttccgctgtt tcttggtttt 180
gcagtaggcc accacacaca tgatgccgac cacaaggagg gcgatgcaga tgccggttat 240
ggtcagcact ctcttctggt acagctcctn cgctncata aattcaatnc caagatgctt 300
gtagaagctg gccattnacg tagttttttg gcagcgattc accagtaaaa cttcatttng 360
gggcac                                     366
```

<210> 191
 <211> 2490
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2490)
 <223> neuregulin 1 (NRG1) gene.

```
<400> 191
gtggctgcgg ggcaattgaa aaagagccgg cgaggagttc cccgaaactt gttggaactc 60
cgggctcggc cggaggccag gagctgag cg gcggcggctg ccggacgatg ggagcgtgag 120
caggacgggtg ataacctctc cccgatcggg ttgcgagggc gccgggcaga ggccaggacg 180
cgagccgccg gcggcgggac ccatcgacga ctcccgggg cgacaggagc agccccgaga 240
gccagggcga gcgccggttc caggtggccg gaccgcccgc cgcgtccgcg ccgcgctccc 300
tgcaggcaac gggagacgcc cccgcgcagc gcgagcgcc cagcgcggcc gctcgctctc 360
cccatcgagg gacaaacttt tccaaaacc gatccgagcc cttggaccaa actcgcttgc 420
gccgagagcc gtccgcgtag agcgcctcgt ctccggcgag atgtccgagc gcaaagaagg 480
cagaggcaaa gggaagggca agaagaagga gcgaggctcc ggcaagaa gc cggagtcgcg 540
ggcgggcagc cagagcccag ccttgccctc ccaattgaaa gagatgaaaa gccagggaatc 600
ggctgcaggt tccaaactag tccttcgggtg tgaaaccagt tctgaatact cctctctcag 660
attcaagtgg ttcaagaatg ggaatgaatt gaatcgaaaa aacaaaccac aaaatatcaa 720
gatacaaaaa aagccaggga agtcag aact tcgcattaac aaagcatcac tggctgattc 780
tggagagtat atgtgcaaag tgatcagcaa attaggaat gacagtgcct ctgccaatat 840
caccatcgtg gaatcaaacg agatcatcac tggtagcca gcctcaactg aaggagcata 900
tgtgtcttca gagtctccca ttagaatata agtatocaca gaaggagcaa atacttcttc 960
atctacatct acatccacca ctgggacaag ccatcttgta aaatgtgcgg agaaggagaa 1020
aactttctgt gtgaatggag gggagtgtct catggtgaaa gacctttcaa acccctcgag 1080
atacttgtgc aagtgcccaa atgagtttac tgggtgatgc tgccaaaact acgtaatggc 1140
cagcttctac aaggcggagg agctgtacca gaagagagtg ctg accataa ccggcatctg 1200
catgcacctc cttgtggteg gcatcatgtg tgtgggtggc tactgcaaaa ccaagaaaca 1260
gcggaaaaag ctgcatgacc gtcttcggca gagccttogg tctgaacgaa acaatatgat 1320
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380
```

125/292

```

tcaatacgtatcttaaaaa cgtcatctccagtgagcatattgttgagagagaagcagagac 1440
atcctttttccaccagtcactatactttccacagcccatcac tccactactgtcaccacagac 1500
tcctagccacagctggagcaacggacacac tgaaagcatcctttccgaaa gccactctgt 1560
aatcgtgatgtcatccgtagaaaacagtaggcacagcagccaaactgggggcccaagagg 1620
acgtcttaatggcacaggag gccctcgtgaatgtaacagcttcctcaggcatgccagaga 1680
aaccctgat tctaccgagactctcctcctatagtgaaggatgtgtcagccatgaccac 1740
cccggctcgtatgtcacctgtagattttccacagccaagctccccaaatcgcccccttc 1800
ggaaatgtctccaccgtgtccagcatgacggtgtccaagccttccatggcggtcagccc 1860
cttcatggaa gaagagagacctctacttctcgtgacacca ccaaggctgcgggagaagaa 1920
gtttgaccatcacctcagcagttcagctccttccaccacaaccccgcgcatgacagtaa 1980
cagcctccctgctagcccttgaggatagtgaggatgagagtatgaaacgaccaaga 2040
gtacgagccagcccaagagcctgttaagaaactcgccaatagccggcgggccaaaagaac 2100
caagcccaatggccacattgctaacagattggaagtggacagcaacacaa gctcccagag 2160
cagtaactcagagtgagagtgaaacagaagatgaagagtaggtgaagatacgcctttcctggg 2220
catacagaaccccctggcagccagtccttgaggcaacacotgcctccgcc tggctgacag 2280
caggactaacccagcaggccgcttctcgacacaggaagaaatccaggccaggtgtctag 2340
tgtaattgctaaccaagaccctattgctgtataaaacctaaataaacacatagattcacc 2400
tgtaaaactttattttatatataaaagtattccaccttaaattaaacaattatttttatt 2460
ttagcagttctgcaataaaa aaaaaaaaaa 2490

```

<210> 192
 <211> 453
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(453)
 <223> 5' terminal sequence. ciliary neurotrophic factor receptor (CNTFR) gene.

```

<400> 192
cagatgctacgccgggaaggagtacattatccaggtggcagccaaggacaatnagattgg 60
gacatggagtgactggagcgtaccgcccacgctacgcctggactgaggaaccgcgacac 120
ctcaccacggaggcccaggctgcggagaccacgaccagcaccaccagctcctggcacc 180
ccacctacca cgaagatctgtgaccctgggagagctgggca gcggcggggg accctcggca 240
cccttcttggtcagcgtccc catcactctg gccctggctg ncgctgccgc cactgccagc 300
agtctcttga tctgagcccg gcaccccatgaggacatgca gagcacctgc agaggancag 360
gaggccggagcttgagcctt gtagaccccggtttctattt tncacacggg caggaggant 420
ttttgcattnttttnagacacaatttttt gga 453

```

<210> 193
 <211> 1566
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1566)
 <223> ciliary neurotrophic factor receptor (CNTFR) gene.

<400> 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgccggcg gaggcctggc ggtgggatcc 60
ggcgggcggt gctagctccg cgctccctgc ctgcctcgct gccgggggag gtcggaaggc 120
gcggcgcgaa gcccggggtg cccgagggcg cgactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtcctg aagagttggt ctggaggagg aggaggacat tgatgtgctt 240
ggtgtgtggc cagtggtgaa gagatggctg ctccctgtccc gtgggcctgc tgtgctgtgc 300
ttgccgccgc cgccgcagtt gtctacgccc agagacacag tccacaggag gcaccccatg 360
tgcagtacga gcgcc tgggc tctgacgtga cactgccatg tgggacagca aactgggatg 420
ctgcggtgac gtggcggtta aatgggacag acctggcccc tgacctgctc aacggctctc 480
agctggtgct ccatggcctg gaactgggcc acagtggcct ctacgcctgc ttccaccgtg 540
actcctggca cctgcgccac caagtcctgc tgcagtgtgg cttgccgcgc cgggagc ctg 600
tgctcagctg ccgctccaac acttacccca agggcttcta ctgcagctgg catctgccc 660
ccccaccta cattccaac accttcaatg tgactgtgct gcattggctcc aaaattatgg 720
tctgtgagaa ggaccagcc ctcaagaacc gctgccacat togtacatg cacctgttct 780
ccaccatcaa gtacaaggtc tccataagtg tcagc aatgc cctggggccac aatgccacag 840
ctatcacctt tgacgagttc accattgtga agcctgatcc tccagaaaat gtggtagccc 900
ggccagtgcc cagcaaccct cgccggctgg aggtgacgtg gcagaccccc tcgacctggc 960
ctgaccctga gtcttttct ctcaagttct ttctgcgcta ccgacccctc atcctggacc 1020
agtggcagca tgtggagctg tccgacggca cagcacacac catcacagat gcctacgccc 1080
ggaaggagta cattatccag gtggcagcca aggacaatga gattgggaca tggagtgact 1140
ggagcgtagc cgccacgct acgcccctga ctgaggaacc gcgacacctc accacggagg 1200
cccaggctgc ggagaccacg accagcacca ccagctccct ggcaccccca c ctaccacga 1260
agatctgtga ccctggggag ctgggcagcg gcgggggacc ctgggcaccc ttcttggtca 1320
ggtccccat cactctggcc ctggctgccg ctgcgcgcac tgccagcagt ctcttgatct 1380
gagcccgga ccccatgagg acatgcagag cacctgcaga ggagcaggag gccggagctg 1440
agcctgcaga ccccggtttc tatttt gcac acgggcagga ggaccttttg cattctcttc 1500
agacacaatt tgtggagacc ccggcgggcc cgggcctgcc gccccccagc cctgccgcac 1560
caagct 1566

```

<210> 194

<211> 349

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(349)

<223> 5' terminal sequence. angiogenin,
ribonuclease, rnase a family, 5 (ANG) gene.

<400> 194

```

ccgtgtacac aactcacac aaggacgcca accccacctg gatgcaaaga ggattcaaaa 60
gaacatcttt gcgttttcta ccggctcccc atcatcgtac tagggaggaa gaagcgggtg 120
agaaacaaaa cttctttcca ttgtcctgcc cgtttctgcg gacttgcttc gaggcgagg 180
agcctgtgtt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttcgtgctgg 240
gtctgggtct gacccaccg acctggctc aggataactn c aggtacaca cacttccctga 300
cccagcacta tgatgcaaaa ccacagggcc nggatgaca gatactgtg 349

```

<210> 195

<211> 729

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(729)
<223> angiogenin, ribonuclease, rnase a family, 5
(ANG) gene.

<400> 195
atgatgccgt gtcagagagc aaagctcctg tccttttggc ctaatttggg gatgctgttc 60
ttgggtctac cacacctcct tttgccctcc gcaggagcct gtgttggaag agatgggtgat 120
gggcctgggc gttttgttgt tgggtcttcgt gctg ggtctg ggtctgaccc caccgaccct 180
ggctcaggat aactccaggt acacacactt cctgaccag cactatgatg ccaaaccaca 240
gggcccggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300
caaagacatc aacacattta ttcattggca caagcgcagc atcaaggcca tctgtgaaaa 360
caagaatgga aacccctcaca gagaaaacct aagaataagc aagtcttctt tccaggtcac 420
cacttgcaag ctacatggag gttccccctg gcctccatgc cagtaccgag ccacagcggg 480
gttcagaaac gttgttgttg cttgtgaaaa tggcttacct gtccacttgg atcagtcaat 540
tttccgtcgt ccgtaaccag cgggccctg gtcaagtgtt ggctctgctg tcct tgcctt 600
ccatttcccc tctgcacca gaacagtggg ggcaacattc attgccaagg gcccaaagaa 660
agagctacct ggaccttttg ttttctgttt gacaacatgt ttaataaata aaaatgtctt 720
gatatcagt 729

<210> 196
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 196
ngttactcca gccttggacc ggggctgcc ctt ggagagn cgtggcgacc acaaggaggc 60
gcacatcctg agggtcctgc cgggccactc ggcggggccc ggacgggtga cgggtgaagg 120
ggaactgagc tgcgcacccg gggatctega tgcgctcctc atcctgcagg gtcccccccta 180
cgtgtcctgg ctcatcgacg ccaaccacaa catgcagatc tggaccactg gagaatactc 240
cttcaagatc ttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300
cctcctgggg ggacgcgn gn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360
taccgctggg ccagcattgt cttnatattc ttgccttcca gottgcgggt gttagggttg 420
cagaccttaa cccgnaccgt ttccagacca tt 452

<210> 197
<211> 379
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(379)
<223> 5' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 197

128/292

```

aggacgagggc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcattg 60
aagacagtcc tatggcttcc tggctcttgag acccggtctt gggacgcagg gctaccgtgc 120
agctgaggggt gccgggttttg ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180
gcgggtcacc ctcgggggctt ggggacagca ggct cacaca gttgcccttg gccgcccggc 240
cctgggatga gttccacggg gcctccctca ggccccaaagt ccagggtggc agctgtctaa 300
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc tttntttgcc 360
ccggcttcga tgggtgtttt                                     379

```

<210> 198

<211> 3142

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)
(ENG) gene.

<400> 198

```

cctggggcggg cggggctgga tgagccgg ga gctccctgct gccgggtcata ccacagcctt 60
catctgcgcc ctgggggccag gactgctgct gtcactgcc tccattggag cccagcacc 120
cctccccgcc catccttcgg acagcaactc cagcccagcc ccgctccct gtgtccactt 180
ctcctgaccc ctcggccgcc accccagaag gctggagcag ggacgccgtc gctccggccg 240
cctgctcccc tggggteccc gtgcgagccc acgcccggcc cggtgcccgc ccgagccct 300
gccactggac acaggataag gccacgcga caggcccca cgtggacagc atggaccgcg 360
gcacgctccc tctggctgtt gccctgctgc tggccagctg cagcctcagc cccacaagtc 420
ttgcagaaac agtccattgt gaccttcagc ctgtgggccc cgagagggg c gaggtgacat 480
ataccactag ccagggtctg aagggtctgc tggctcaggc cccaatgcc atccttgaag 540
tccatgtcct ctctctggag ttcccaacgg gcccgtcaca gctggagctg actctccagg 600
catccaagca aaatggcacc tggccccgag aggtgcttct ggtcctcagt gtaaacagca 660
gtgtcttctt gcctctccag gccctgg gaa tcccaactgca cttggcctac aattccagcc 720
tggtcacctt ccaagagccc ccgggggtca acaccacaga gctgccatcc ttccccaaga 780
cccagatcct tgagtgggca gctgagaggg gcccacac ctctgctgct gagctgaatg 840
acccccagag catcctctc cgactgggccc aagcccaggg gtcactgtcc ttctgcatgc 900
tggaagccag ccaggacatg ggccgcacgc tgcagtggcg gccgcgtact ccagccttgg 960
tccggggctg ccacttgga ggcggtggcc gccacaagga ggcgcacatc ctgagggtcc 1020
tgccggggcca ctcggccggg ccccgacgg tgacggtgaa ggtggaactg agctgcgcac 1080
ccggggatct cgatgcctgc ctcatcctgc aggtccccc ctacg tgtcc tggctcatcg 1140
acgccaacca caacatgcag atctggacca ctggagaata ctcttcaag atctttccag 1200
agaaaaacat tctgtggttc aagctcccag acacacctca aggcctcctg ggggaggccc 1260
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ccgacgacgc catgacctg gtactaaaga aagagcttgt tgcgcatttg aagtgcacca 1500
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gcaaaggcct cgtcctgccc gccgtgctgg gcatcacctt tggtgcttc ctcatcgggg 2160
ccctgctcac tgtctgactc tggtagatct actcgcacac gcgtgag tac cccaggcccc 2220

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```

cacagtgage atgccggggc cctccatcca cccggggggag cccagtgaag cctctgaggg 2280
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ccccagcaa gcgggagccc gtggtggcgg tggctgcccc ggcctcctcg gagagcagca 2400
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cagcccagcc aggccaacag cacctccccg ctggg aagag aagagggccc agcccagagc 2880
cacctggatc tatccctgcg gcctccacac ctgaacttgc ctaactaact ggcaggggag 2940
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tgaaacctga aaaaaaaaaa aa 3142

```

<210> 199
 <211> 402
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(402)
 <223> 3' terminal sequence. epidermal growth
 factor (beta-urogastrone) (EGF) gene.

```

<400> 199
tatgtttttg gtgattttat ttaaataatt agaagaaatt catcgttgtc tataatgaaa 60
acaaatcagg caatttactt acaatcttgt aactgaaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa aaggacagta atgactaaga aactccgaag 180
cctcctgtgt aatatittta aaataaaatg ttttcattca aatatittta aaaataagcc 240
atctaattct gaagaaatca gtttctaaat tacatttttc attgattcat cacaactcat 300
tttgcaaaat catcagcatg gaccagc cca atgaggagtt aaatgcctac actgtatctt 360
aacggtattg taatattcca atcatttcat gaaactgata ta 402

```

<210> 200
 <211> 4877
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(4877)
 <223> epidermal growth factor (beta -urogastrone)
 (EGF) gene.

```

<400> 200
actgttggga gaggaatcgt atctccatat ttcttctttc agccccaatc caagggttgt 60
agctggaact ttccatcagt tcttctttc ttttctctct ctaagccttt gccttgcctc 120
gtcacagtga agtcagcca g agcagggtc ttaaactctg tgaaatttgt cataagggtg 180
tcaggtattt cttactggct tccaaagaaa catagataaa gaaatctttc ctgtggcttc 240

```

ccttggcagg ctgcattcag aaggtctctc agttgaagaa agagcttggg ggacaacagc 300
 acaacaggag agtaaaagat gccccagggc tgaggcctcc gctcaggcag ccgcatctgg 360
 ggtcaatcat actcaccttg cccggggccat gctccagcaa aatcaagctg ttttcttttg 420
 aaagttcaaa ctcatcaaga ttatgtctgt cactcttata attctgttgc cagtagtttc 480
 aaaatttagt tttgttagtc tctcagcacc gcagcactgg agctgtcctg aaggctactct 540
 cgcaggaaat gggaattcta cttgtgtggg tcctgcacc c tctttaattt tctcccatgg 600
 aaatagtatc tttaggattg acacagaagg aaccaattat gagcaattgg tgggtgatgc 660
 tgggtgtctc gtgatcatgg attttctatta taatgagaaa agaactctatt ggggtgattt 720
 agaaagacaa cttttgcaaa gagtttttct gaatgggtca aggcaagaga gagtatgtaa 780
 tatagagaaa aatgttt ctg gaatggcaat aaattggata aatgaagaag ttatttgggtc 840
 aaatcaacag gaaggaatca ttacagtaac agatatgaaa ggaaataatt cccacattct 900
 tttaaagtct ttaaaatata ctgcaaatgt agcagttgat ccagtagaaa ggtttatatt 960
 ttggtcttca gaggtggctg gaagccttta tagagcagat ctgatgggtg tgggagtga a 1020
 ggctctgttg gagacatcag agaaaataac agctgtgtca ttggatgtgc ttgataagcg 1080
 gctgttttgg attcagtaca acagagaagg aagcaattct cttatttggc cctgtgatta 1140
 tgatggaggt tctgtccaca ttagtaaaaca tccaacacag cataatttgt ttgcaatgtc 1200
 cctttttggg gaccgtatct tctattcaac atg gaaaatg aagacaattt ggatagccaa 1260
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 ctgtgaagat gttaatgaat gtgctttttg gaatcatggc tgtactcttg ggtgtaaaaa 1560
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 aaaaagctgt gcagcttcag g accacaacc attttctgctg tttgccaatt ctcaagatat 1920
 tcgacacatg cattttgatg gaacagacta tggaaactctg ctacagccagc agatgggaat 1980
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 agtagatgtg ccagaaggtc ttgctgtgga ctggatggc cgtagattct attggacaga 2160
 cagagggaaa tctctgattg gaaggagtga tttaaatggg aaacgttcca aaataatcac 2220
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 tgacaagtgt tactggtgcg atgccaagca gtctgtgatt gaaatggcca atctggatgg 2460
 ttcaaaacgc cgaagactta ccagaaatga tgtagggtcac ccatttgcct tagcagtgtt 2520
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 ggttcatcca ttggcaaaac caggagcaga tccctgctta tatcaaaacg gaggctgtga 2700
 acatatattg aaaaagaggc ttggaactgc ttggtgttgc tgtcgtgaa g gttttatgaa 2760
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 gtaccgagac ctgaagtggg gggaactgcg ccacgtctgg cacgggcagc agcagaagggt 3540
 catcgtgggt gctgtctgcg tgggtgggtg tgtcatgctg ctctctctga gcctgtgggg 3600
 ggcccactac tacaggactc agaagctgct atcgaaaaac ccaaagaatc cttatgagga 3660
 gtcgcagaga gatgtgagga gtcgcaggcc tctgacact gaggatggga tgtcctcttg 3720
 cctcaacctt tggtttggg ttataaaaga acaccaagac ctcaagaatg ggggtcaacc 3780
 agtggctggg gaggatggcc aggcagcaga tgggtcaatg caaccaactt catggaggca 3840
 ggagccccag ttatgtggaa tgggcacaga gcaaggctgc tggattccag tatccagtga 3900

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taagggctcc tgtccccagg taatggagcg aagctttcat atgccctcct atgggacaca 3960
gacccttgaa gggggtgtcg agaagcccca ttctctccta tcagctaacc cattatggca 4020
acaaagggcc ctggaccac cacac caaat ggagctgact cagtgaaaac tggaattaaa 4080
aggaaagtca agaagaatga actatgtcga tgcacagtat cttttctttc aaaagtagag 4140
caaaactata ggttttggtt ccacaatctc tacgactaat cacctactca atgcctggag 4200
acagatacgt agttgtgctt ttgtttgctc ttttaagcag tctcactgca gtcttatttc 4260
caagtaagag tactgggaga atcactaggt aacttattag aaacccaaat tgggacaaca 4320
gtgctttgta aattgtgttg tcttcagcag tcaatacaaa tagatttttg tttttgttgt 4380
tcctgcagcc ccagaagaaa ttaggggtta aagcagacag tcacactggt ttggtcagtt 4440
acaaagtaat ttctttgatc tggacagaac atttatatc a gtttcatgaa atgattggaa 4500
tattacaata ccgttaagat acagtgtagg catttaactc ctcatggcg tgggccatgc 4560
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aaatattaca caggaggcct tcggagtttc ttagtcatta ctgtcctttt cccctacaga 4740
atTTTccctc ttggtgtgat tgcacagaat ttgtatgtat tttcagttac aagattgtaa 4800
gtaaattgcc tgatttgttt tcattataga caacgatgaa tttcttctaa ttattttaaT 4860
aaaatcacca aaacat 4877

```

<210> 201
 <211> 153
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(153)
 <223> 3' terminal sequence. hmt1 (hnrnp
 methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
 gene.

```

<400> 201
attagacctc acattagggga aaacatcaaa atgantcacg cacgaccctt gagatcctga 60
ggttggccca gccgagcccg tgctcagaag cccccagct ccggcccca gctgcccga 120
cgccgcctt caccagcagg caggtcccca tcc 153

```

<210> 202
 <211> 472
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(472)
 <223> 5' terminal sequence. hmt1 (hnrnp
 methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
 gene.

```

<400> 202
agtgaatcgc agggagaaga gcctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgtg ccaccgatga gaccagctc 120
agttttttga gaggagaaaa aattcttatt ctgagacaaa ccaactgcaga ttggtggtgg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggcaaacc atgtggggaa gcacgtggat 240
gagtacgacc ccgaggacac gtggcaggat gaagagtact tcggcagcta tggaaactctg 300

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```

aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttcctgncag gaattaaaga atccctgnac ggnttaaagt tcttcnnggg acgtggggct 420
gtggggattt gggatccttc agtctcttnt tgttgccacat tttgcgtggc nt 472

```

<210> 203

<211> 2093

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2093)

<223> hmt1 (hmrnp methyltransferase, s.
cerevisiae)-like 1 (HRMT1L1) gene.

<400> 203

```

cactgcgctt gcgcgggttg agggcggttg ctcagtctcc tggaaaggac cgtccacccc 60
tccgcgcttg cgggtgtggac gcggaactca gcggagaaac gcgattgaga aatggaaaag 120
aaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcaggt 180
gactgtccca gaagtgaatc gcaggagaaa gagcctgctg agtgcagtga ggcgggtctc 240
ctgcaggagg gactacagcc agaggagttt gtggccatcg cggactacgc tgccaccgat 300
gagaccacgc tcagtttttt gagaggagaa aaaattctta tcctgagaca aaccactgca 360
gatttgttgtt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgtgg atgagtacga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
tatggaactc tgaaactcca cttggagatg ttggcagacc agccacgaac aactaaatac 540
cacagtgtca tcctgcagaa taaagaatcc ctgacggata aagtcacctt ggacgtgggc 600
tgtgggactg ggatcatcag tctcttctgt gcacactatg cgcggcctag agcgggtgtac 660
gcggtggagg ccagtgaagt ggcacagcac acggggcagc tggctcctga gaacggcttt 720
gctgacatca tcaccgtgta ccagcagaag gtggaggatg tgggtgctgc cgagaagggtg 780
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gccgacccgt ggctgggtcg gagctccatg ttctaagct aggtctaggt ctacactcct 1800
aggacgcacg catatcagcc cgtgtacctg gtgacagtga ctgtcccccac ctctgtgtt 1860
agtgtgccc ttactgccgt cgctcatoca ctctgtggg acgtaggatt gcaca gggct 1920
gtgccagtgg cgtgtaggga acaactgccct ggctcagcgt gcgagctaag gtggcgatgt 1980
atgcgatggg actctgcatg ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttggtgcc atcgcacatg ctcaataaat attttaaatg agtgaaaaaa aaa 2093

```

<210> 204

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

```
tggggggcctt tatta aggtc tggcagatgt ggtggaggtg gaagtacaaa cccaggcctg 60
ggcctaggaag agggcagaag aaaggcaaag ggtcccttgg agcaggaacc catccctctc 120
tgcttatacc cagcaccctt catcccaggt tcctttcttc aacctccgcc tgcctctggg 180
aacacagagc accaagaact gacaaaccgg gaccctccag gggccacagc gtgggggc ag 240
agtccaggn ttctgtctcc ccgcagtggg gagatctngg ggagctcagg tgaacctcct 300
cancctcctg ccagtatgaa gttggggaag cgccttttct tgtccccag aacagaacaa 360
actctgttc tctgtgggtt ngggggaaaa ggtttngggg ggtttgact taggggagaa 420
gttnagcttg a 431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

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gtccccctgcc cctgcccttg gacagtcgcc cctacagncc tttccccggg cagagaacgg 60
aatttcctga gatcctcttg cacctcccag cccaccctg gccatgggta cctcggggaa 120
catagctccg tcttccagca gcccctggga catttgccac tccttcacat ctcaggagg 180
gggccgggaa cccctcccag gcccctacc aacaccagct gtggagccc tgcccaccct 240
atccccagca gagctttaag caagaatacc atgatccct gtatggaaca gggnggggcc 300
agccaggccg tgggaaccag ggggtggggg tcaatggggg cacagggtac ccaggggggn 360
gggggggttg ttgattcaaa acagggaaca gacgggattt tt ggnnttaag gatttnaggt 420
tntttaancg gggtg 435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)
gene.

<400> 206

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```

agaccccagt cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt cccgcagcaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttcga agcgacacat 180
cagggcactt ccagcggctc ctcatctctc tctctcaggg aaaccgtgat gaaagcacaa 240
acgtggacat gtcactcgcc cagagagatg cccagggagc tgtatgcggn ccggggagaa 300
ccgcctgggg aacagacgag tccaagtttc aattgcggtt tctgtggctt cccgggagcc 360
gggcncacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggccnggac 420
atttntagaa gagcatctgc ccggaga 447

```

<210> 207

<211> 1958

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1958)

<223> annexin all (ANXA11) gene.

<400> 207

```

gctgctgcgc ccgcggctcc ccagtgcgcc gagtgcgccg cgggccccgc gagcgggagt 60
gggaccagc cctaggcaga acccaggcgc cgcgcccggg acgcccgcgg agagagccac 120
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<210> 208

<211> 433

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(433)
 <223> 5' terminal sequence. platelet-derived
 growth factor receptor, beta polypeptide (PDGFRB)
 gene.

<400> 208
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 taccccaag gag 433

<210> 209
 <211> 5570
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5570)
 <223> platelet-derived growth factor receptor,
 beta polypeptide (PDGFRB) gene.

<400> 209
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<210> 210

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 5' terminal sequence. williams-beuren
syndrome chromosome region 14 (WBSR14) gene.

<400> 210

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aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
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accagatgcg agacatgttt gatggactac gtccgaacc gtacgctgca caa ctgggaa 360
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<210> 211

<211> 3293

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3293)

<223> williams-beuren syndrome chromosome region
14 (WBSR14) gene.

<400> 211

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<210> 212

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(207)

<223> 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility
complex, class ii antigen-associated) (CD74) gene.

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<400> 212

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gacccctagt tccctctgct cagccaagct tggtatcagc tttcagggcc atngttcaca 180
ttagaataaa aggtagtaat taganaa 207
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<210> 213

<211> 1304

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1304)

<223> cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

<400> 213

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<210> 214

<211> 355

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(355)

<223> 5' terminal sequence. annexin a7 (ANXA7) gene.

<400> 214

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aggaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60
ggcaatgaag ggttttggga cagatgagca ggcaattgtn gatgtngttg ccaaccggtt 120
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctccataggc aaggatttaa 180
tcaaagatct caaatcagag ttaagtngaa atatggaaga actgatcctn ggccctcttc 240
atgcctccta cgtattacga tgcctngagc ttacggaaga gcaatncagg gancaggta 300
tcaggancgt tgtatttgat ttgngatttt ngtgcacang atcanattca ggtaa 355

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<210> 215

<211> 2176

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2176)

<223> annexin a7 (ANXA7) gene.

<400> 215

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gaacccggtc tcccgaaga tggagccggg ttgggctgtg acgctgctgc tggggtcaga 60
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ataaaaaatt gcatat 2176

```

<210> 216
 <211> 525
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(525)
 <223> 3' terminal sequence. thrombospondin 1
 (THBS1) gene.

<400> 216
 tcctgnanta nctncaacaa ccgatgtgag ggaaaatcgg tccagacacg gacctgccac 60
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 tcatcttggt ctgtgacatg tggatgatgt gtgatcaca ggatccggct ctgcaactct 180
 ccagccccc agatgaacgg gaaacctgt gaaggcgaag gcgngagac caaagcctgc 240
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 tctttttaat tgaaaaacaa attcacntt ttccccagct ttttttcctt gtgttcaggg 480
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<210> 217
 <211> 5722
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5722)
 <223> thrombospondin 1 (THBS1) gene.

<400> 217
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143/292

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```

<210> 218

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 218

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ttaatgctgc caaaaagtat aaaaatacag taggaatggc agtacaatac aaagtaatct 60
ctcctaattt atttcttgta catctttcta catttcatac actcattaac aacacttaac 120
acatccaatt aaagggtctg caaagtcttc tgctggtggg tgctcttcat cccctgggnt 180
gtaaaagttta ctttgtaaac aaacaactgt gaggncaatc tagagggtta gccgagcctc 240
actttagttt ccggagtggg gcttcagggc cttgctttgc acatcaatgg gttcaaaaatt 300
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<210> 219

<211> 338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(338)

<223> 5' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 219

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ggctccttga accctgacca tgggcctgcg gtgatccact gtagtgcagg cattgggcgc 60
tctggcacct tctctctggt agacacttgt cttgttttga tggaaaaagg agatgatatt 120
aacataaaac aagtgttact gaac atgaga aaataccgaa tgggtcttat tcagacccca 180
gatcaactga gattctcata catggctata atagaaggag caaaatgtat aaaggagat 240

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tctagtatac agaaacgatg gaaagaactt tctaaggang acttatctcc tgcctttgat 300
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<210> 220

<211> 2287

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2287)

<223> protein tyrosine phosphatase, non -receptor
 type 2 (PTPN2) gene.

<400> 220

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atcacaggat ttgttttttg aggctatctg gatttttaacc tgcacttgat ataagcaata 1680
aatattgtgg ttttatctac gttatttgaa agaaaatgac atttaaataa tgtgtgtaat 1740
gtataatgta ctattgacat gggcatcaac acttttatc ttaagcattt cagggtaaat 1800
atattttata agtatctatt taatcttttg tagttaactg tactttttta gagctcaatt 1860
tgaaaaatct gttactaaaa aaaaaaattg tatgtcgatt gaattgtact ggatacattt 1920
tccatttttc taaaaagaag tttgatatga gcagttagaa gttggaataa g caattttcta 1980
ctatatattg cattttcttt atgtttttaca gttttcccca ttttaaaaag aaaagcaaac 2040
aaagaacaaa aagtttttcc taaaaatatc tttgaaggaa aattctcctt actgggatag 2100
tcaggtaaac agtttggtcaa gactttgtaa agaaattggg ttctgtaaat cccattattg 2160
atatgtttat ttttcatgaa aatttc aatg tagttggggg agattatgat ttaggaagca 2220
aaagtaagaa gcagcatttt atgattcata atttcagttt actagactga agttttgaag 2280
taaacc 2287

```

<210> 221

<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(296)
<223> 3' terminal sequence. epha2 (EPHA2) gene.

<400> 221
ctcggctggc tcacacaccc gtatggcaaa ggggtgggacc tgatgcagaa catcatgaat 60
gacatgccga tctacatgta ctccgtgtgc aacgtgatg t ctggcgacca gganaactgg 120
ctccgcacca actgggtgta ccgaggagag gctgagcgt tcttcattga gctcaagttt 180
actgtactgt actgcaacag cttccctggg tggcgccant tcctggcaag gagactttca 240
acctctacta tgccgagtcg gacctgggac tacggcanca acttncagaa gcgcct 296

<210> 222
<211> 3921
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3921)
<223> epha2 (EPHA2) gene.

<400> 222
cggaagtgtc ggcgaggccg gcggggcgga ggggacaccg aggcggcggt gcaggcgtgc 60
gggtgtgcgg gagccgggct cggggggatc ggaccgagag cgagaagcgc ggcatggagc 120
tccaggcagc ccgcgcctgc ttccgccctgc tgtggggctg tgogctggcc gcggccgcgg 180
cggcgagagg caaggaagtg gtactgctgg actttgctgc agctggaggg gagctcggct 240
ggctcacaca cccgtatggc aaaggggtggg acctgatgca gaacatc atg aatgacatgc 300
cgatctacat gtactccgtg tgcaacgtga tgtctggcga ccaggacaac tggtcccgca 360
ccaactgggt gtaccgagga gaggctgagc gtaacaactt tgagotcaac tttactgtac 420
gtgactgcaa cagcttccct ggtggcgcca gctcctgcaa ggagacttcc aacctctact 480
atgccgagtc ggacctggac tacgg cacca acttccagaa gcgcctgttc accaagattg 540
acaccattgc gcccgatgag atcacgctca gcagcgactt cgaggcacgc cacgtgaagc 600
tgaacgtgga ggagcgctcc gtggggccgc tcaccgcga aggcttctac ctggccttcc 660
aggatatcgg tgccctgtgtg gcgctgctct ccgtccgtgt ctactacaag aagtgcctcg 720
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tgccctgcac acgaccccc tccgccccac actacctcac agccgtgggc atgggtgcca 1140
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gcgtcacctg cgaacagtgc tggcccgagt ctggggaatg cgggccgtgt gaggccagt 1260
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agagccgagt gtggaagtac gaggtcactt accgcaagaa gggagactcc aacagctaca 1560
atgtgcgccg caccgagggg ttctccgtga ccct ggacga cctggcccca gacaccacct 1620

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acctggtcca ggtgcaggca ctgacgcagg agggccaggg ggccggcagc aaggtgcacg 1680
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tcggtgtggt cctgcttctg gtgctggcag gagttggctt ctttatccac cgcaggagga 1800
agaaccagcg tgcccgccag tccccggagg acgtttactt ctccaagtca gaacaactga 1860
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agttcactac cgagatccat ccatacctgtg tcactcggca gaaggtgatc ggagcaggag 1980
agtttgggga ggtgtacaag ggcattgctga agacatcctc ggggaaga ag gaggtgcccg 2040
tggccatcaa gacgctgaaa gccggctaca cagagaagca gcgagtggac ttctcggcg 2100
aggccggcat catggggccag ttacagccacc acaacatcat ccgcctagag ggcgtcatct 2160
ccaaatacaa gcccatgatg atcatcactg agtacatgga gaatggggcc ctggacaagt 2220
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tcgcagctgg catgaagtac ctggccaaca tgaactatgt gcaccgtgac ctggctgccc 2340
gcaacatcct cgtcaacagc aacctggtct gcaagggtgtc tgactttggc ctgtcccgcg 2400
tgctggagga cgaccccgag gccacctaca ccaccagtgg cggcaagatc cccatccgct 2 460
ggaccgcccc ggaggccatt tcctaccgga agttcacctc tgccagcgac gtgtggagct 2520
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accacgaggt gatgaaagcc atcaatgatg gcttcgggct cccacacccc atggactgcc 2640
cctccgccat ctaccagctc atgatgcagt gctggc agca ggagcgtgcc gcccgcccca 2700
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tgggactcaa ggaccaggtg aacactgtgg ggatecccat ctgagcctcg acagggcctg 3060
gagccccatc ggccaagaat acttgaagaa acagagtggc ctccctgctg tgccatgctg 3120
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ctggagcagg agccccgcca cagc cttcgg acagacatat aggatattcc caagccgacc 3360
ttccctccgc cttctcccac atgaggccat ctccaggagat ggagggcttg gccagcgcc 3420
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gtgttgaggt ttttaaatat atattttgt a ctttgtggag agaattgtgtg tgtgtggcag 3660
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ataagtttct attctgtcag tgttaaagat tttgttttgt tggacatttt tttcgaatct 3840
taattttatta ttttttttat atttattgtt agaaaatgac ttattttctgc tctggaataa 3900
agttgcagat gattcaaacc g 3921

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<210> 223

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1) gene.

<400> 223

```

ggaacagggt ggacactgtg caggcttcag cttccactcc gggcaggatt caggctatct 60
gggaccgcag gacttgccag gngcacagcc ctggctcccg aggcaggcag gcaagggtgac 120
gggactggaa gcccttttca naggccttga ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggg atggataaac agggaaacac tgtgcattcc tcacagccaa 240

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cagtntaggt cttggtnaag ccccggcgct gagctaagct caggcttttc caggggagcc 300
acgaaactnc aggtagtgat gtgcaagagt ccatacctgca gttttccagc aatnagaaac 360
tcctcgttng cggtttttgg ggaccnttgg aagtnttc cg cagacatttt tccatgggcc 420
gggttttaag acgaacc                                     437

```

<210> 224

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of
metalloproteinase 1 (erythroid potentiating
activity, collagenase inhibitor) (TIMP1) gene.

<400> 224

```

gccncagatc cagcgcccag agagacacca gagaaccac catggccccc tttgnagccc 60
ctggcttctg gcatacctgtt gttgctgtgg ctgatagccc ccagcagggc ctgcacctgt 120
gtcccacccc acccacagac ggccttctgc aattccgacc tcgtcatcag ggccaagttc 180
gtggggacac cagaagtcaa ccagaccacc ttataccagc gttatgagat caagatgacc 240
aagatgtata aagggttcca agccttaggg gatgcgctg acatccgggt cgtctacacc 300
cccgccatgg agagtgtctg cggatacttn cacagggtccc acaaccgnag cgaggagttt 360
ctcattngct ggaaaactgt aggatggact tcttgacat tnactacctt gcagttttng 420
tgggttcctt gggaacagtc tgagggtttag tttagcggtt ggggtt                466

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<210> 225

<211> 782

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(782)

<223> tissue inhibitor of metalloproteinase 1
(erythroid potentiating activity, collagenase
inhibitor) (TIMP1) gene.

<400> 225

```

aggggcctta gcgtgccgca tcgcagagat ccagcgccca gagagacacc agagaaccca 60
ccatggcccc ctttgagccc ctggcttctg gcatacctgtt gttgctgtgg ctgatagccc 120
ccagcagggc ctgcacctgt gtcccacccc acccacagac ggccttctgc aattccgacc 180
tcgtcatcag ggccaagttc gtggggacac cagaagtcaa c cagaccacc ttataccagc 240
gttatgagat caagatgacc aagatgtata aagggttcca agccttaggg gatgcgctg 300
acatccgggt cgtctacacc cccgccatgg agagtgtctg cggatacttc cacagggtccc 360
acaaccgcag cgaggagttt ctcattgctg gaaaactgca ggatggactc ttgcacatca 420
ctacctgcag tttcgtggct ccctggaaca gcctgagctt agctcagcgc cggggcttca 480
ccaagaccta cactgttggc tgtgaggaat gcacagtgtt tcctgttita tccatcccct 540
gaaaactgca gagtggcact cattgcttgt ggacggacca gctcctccaa ggctctgaaa 600
agggcttcca gtcccgtcac cttgcctgcc tgccctcgga gccagggtct tgcacctggc 6 60
agtcctgcg gtcccagata gcctgaatcc tgcccggagt ggaactgaag cctgcacagt 720
gtccaccctg ttcccactcc catctttctt ccggacaatg aaataaagag ttaccaccca 780

```

gc

782

<210> 226
 <211> 353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(353)
 <223> 5' terminal sequence. ephrin-a1 (EFNA1)
 gene.

<400> 226
 acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60
 tgaagggtgac tgtcagtggc aaaatcactc acagtccctca ggcccatgtc aatccacagg 120
 agaagagact tgcagcagat gaccagagg tgccgggttct acatagcatc ggtcacagtg 180
 ctgccccacg cctcttccca cttgcctgga ctgtgctgct ccttccactt ctgctgctgc 240
 aaaccccggtg aagggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300
 caggcactcc aaacctgtct tggggggccac tttagagagcc ccagccctt ggg 353

<210> 227
 <211> 1480
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1480)
 <223> ephrin-a1 (EFNA1) gene.

<400> 227
 gcggagaaag ccagtgggaa ccagaccca taggagacc gcgtccccgc tcggcctggc 60
 caggccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120
 cgctgctgat cgccacaccg tcttctggaa cagttcaa atccaagttcc ggaatgagga 180
 ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
 tcaactctgtg gcagacgtg ccattggagca gtacatactg tacctgggtg agcatgagga 300
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 tgccaagcat ggcccgga agctgtctga gaagttccag cgcttcacac ctttcaccct 420
 gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
 tgaagaccgc tgcttgaggt tgaagggtgac tgtcagtggc aaaatcactc acagtccctca 540
 ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgccgggttct 600
 acatagcatc ggtcacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660
 ccttccactt ctgctgctgc aaaccccggtg aagggtgtatg ccacacctgg ccttaaagag 720
 ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttcagagccc 780
 ccagccctgg gaaccactcc caccacaggc ataagctatc aactagcagc ctcaaaacgg 840
 gtcagtatta aggttttcaa ccggaaggag gccaaccagc ccgacagtgc catccccacc 900
 ttcacctcgg agggacggag aaagaagtgg agacagtcc tttccaccat tcctgccttt 960
 aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020
 aagggggcac gtggatgggc aaagcttgtc aaagatgcc cctccag gag agagccagga 1080
 tgcccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140
 caggagaggc agcatgcttg ggctgaccca gcattctcca gcaagacctc atctgtggag 1200
 ctgccacaga gaagtttcta gccaggctact gcattctctc ccattcctgg gcagcactcc 1260

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ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgcccatg tgtacattct gcctagagtg tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaaat aaagcaatgt gttttttcgg 1480

```

<210> 228

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(170)

<223> 3' terminal sequence. endothelin receptor
type a (EDNRA) gene.

<400> 228

```

ttttaagggtt tctgtaaact tttatttttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca aagttacttg ttgaaaagat gtagtaaagg tagaaattgg 120
aaatattcct gctagtaaac cacagttact taccagtcca taaataaaat 170

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<210> 229

<211> 4105

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4105)

<223> endothelin receptor type a (EDNRA) gene.

<400> 229

```

gaattcgcgg ccgcctcttg cgggtcccaga gtggagtgga aggtctggag ctttgggagg 60
agacggggag gacagactg g aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcac cgcgtggtct gacgattgtg gagaggcggg ggagaggcct 180
catccatccc acccggtcgt cgccggggat tgggggtccc gcgacacctc cccgggagaa 240
gcagtgcaca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgccgcg 300
cggagcccgg gacaccggcc accctccggc ccacccacct tcgctttctc cggcttccctc 360
tgccccaggc gccgcgcgga cccggcagct gtctggcgac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttcctc aaatttgcct 480
caagatggaa accctttgcc tcagggcatc cttttggct g gcaactgggtg gatgtgtaat 540
cagtataaat cctgagagat acagacacaa tctaagcaat catgtggatg atttcaccac 600
ttttcgtggc acagagctca gcttcctggt taccactcat caaccacta atttggtcct 660
accagcaat ggctcaatgc acaactattg cccacagcag actaaaatta cttcagcttt 720
caaatacatt aacactg tga tatctgtac tttttcatc gtgggaatgg tggggaatg 780
aactctgctc aggatcattt accagaacaa atgtatgagg aatggcccca acgcgctgat 840
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tgaagcgatt ggcttcgtca tggtaacctt tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgctcaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260

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cttcgggttc tatttctgta tgcccttgggt gtgcactgog atctttctaca ccctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtcga gaagtggcaa aaacagtttt ctgcttgggt gtaatttttg ctctttgctg 1440
gttccctctt cacttaagcc gtatattgaa gaaaactgtg tataacgaaa tggacaagaa 1500
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ctggtttatc caccacaac atctacgaat cgtacttctt taattgatct aatttacata 1980
ttctgctgtg tgtattcagc actaaaaaat ggtgggagct gggggagaat gaagactgtt 2 040
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atggtgtttt attacaaggg accttgaaca tgttttgtat gttaaattca aaagtaatgc 2580
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aaaatcaatg tcaagtacca aaatgttaat gtatgtgtca ttttaactctg cctgagactt 2700
tcagtgcact gtatatagaa gtctaaaaca cacctaagag aaaaagatcg aatttttcag 2760
atgattcgga aattttcatt cagggtattt taatagtac atatatatgt atatacata 2820
cacctcctat tctcttaatt tttgttaaaa tgttaactgg cagtaagtct tttttgatca 2880
ttcccttttc catataggaa acat aatttt gaagtggcca gatgagtta tcatgtcagt 2940
gaaaaataat taccacaaa tgccaccagt aacttaacga ttcttcaactt cttgggggtt 3000
tcagtatgaa cctaactccc caccocaaca tctccctccc acattgtcac catttcaaag 3060
ggcccacagt gacttttgc tggcattttt ccagatgttt acagactgtg agtacagcag 312 0
aaaatctttt actagtgtgt gtgtgtatat atataaaca ttgtaaattt ctttttagccc 3180
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ggtatgtatg gatttaattc aatctaataa ttgtgccccg cagttgtgcc aaagtgcata 3300
gtctgagcta aaatctaggt gattgttcat catgaca cc tgcctcagtc catttttaacc 3360
tgtagcaacc ttctgcattc ataaatcttg taatcatgtt accattacaa atgggatata 3420
agaggcagcg tgaaagcaga tgagctgtgg actagcaata taggggtttt tttggttgg 3480
tggtttgata aagcagtatt tggggtcata ttgtttcctg tgctggagca aaagtcatta 3540
cactttgaag ta ttatattg ttcttatcct caattcaatg tggatgatga attgccaggt 3600
tgtctgatat ttctttcaga ctlogccaga cagattgtctg ataataaatt aggtaaagata 3660
atgtgttggg ccatatttta ggacaggtaa aataacatca ggttcagtt gcttgaattg 3720
caaggctaag aagtactgcc cttttgtgtg ttagcagtoa aatctattat t ccaactggcg 3780
catcatatgc agtgatatat gcctataata taagccatag gttcacacca ttttgtttag 3840
acaattgtct ttttttcaag atgctttgtt tctttcatat gaaaaaaatg cattttataa 3900
attcagaaag tcatagattt ctgaaggcgt caacgtgcat tttatttatg gactggtaag 3960
taactgtggt ttactagcag gaatat ttcc aatttctacc tttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg ccataagt 4080
taaaataaaa gtttacagaa acctt 4105

```

<210> 230

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 230
ggtttcttgt tttttattat tggcgtcagt agngactata cgtggcctta aacgtcatgc 60
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180
atccaacgcc ccctcccacc ccctaaagtt ccaaccaaag tgagaggggc acagggtgac 240

<210> 231
<211> 475
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(475)
<223> 5' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 231
cttaaatggaa aagacggcctt cattcccaag aactacatag aaatga aacc acatccgtgg 60
tttttttgca aaatccccag agccaaggca gaagaaatgc ttagcaaaca gcggcacgat 120
ggggcctttc ttatccgaga gagtgcagag gctcctgggg acttctccct ctctgtcaag 180
tttgaaaacg atgtgcagca cttcaagggtg ctccgagatg gagccgggaa gtacttcctc 240
tggtgtgtga agttcaattc ttgga atgag ctggtggatt atcacagatc tacatctgtc 300
tccagaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360
atacgttcca ggggcctttt ttgattttt gattccccag gggggnnttg ngagggtggg 420
ttttccgccg ggggagattt tattccatgt tcntgggtn aatttaggaa cntt 475

<210> 232
<211> 1109
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1109)
<223> growth factor receptor-bound protein 2
(GRB2) gene.

<400> 232
gccagtgaat tcgggggctc agccctcctc cctcccttcc cctgcttca ggctgctgag 60
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120
gacgagctga gcttcaaaaag gggggacatc ctcaagggtt tgaacgaaga atgtgatcag 180
aactggtaca aggcagagct taatggaaaa gacggcttca ttcccaagaa ctacatagaa 240
atgaaaccac atccgtgggt ttttggcaaa atccccagag ccaaggcaga agaaatgctt 300
agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360
ttctccctct ctgtcaagtt tggaaacgat gtgcagcaat tcaagggtgct ccgagatgga 420
gccgggaagt acttctctct ggtggtgaag ttcaattctt tgaatgagct ggtggattat 480
cacagatcta catctgtctc cagaaaccag cagatattcc tgccgggacat agaacagggtg 540
ccacagcagc cgacatacgt ccaggccctc tttagactttg atccccagga ggatggagag 600
ctgggcttcc gccggggaga ttttatccat gtcattggata actcagaccc caactggttg 660

152/292

```

aaaggagctt gccacggg ca gaccggcatg tttccccgca attatgtcac ccccgatgaac 720
cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tggccgggtc accctgtgac cctctcactt tgggttgaac tttaggggggt gggaggggggc 900
gttggattta aaaatgccaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tcactgctgc tcctcttttc cctcctttgt cttttttttt atcctttttt ctcttctgtc 1020
catcagtgc tgacgtttta ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaaccaa aaaaaaaaaa ccgaattca 1109

```

<210> 233

<211> 446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene
(JUND) gene.

<400> 233

```

cgcgctctc ggctgccnng ntgtacaccg cgccggaaag tggggctccg agggggcgca 60
ctcaaaaccc tgcctttcct ttacttttac tttttttttt tttcttttg aagagagaag 120
aacagagtgt tcgattctgc cctatttatg tttctactcg ggaacaaaac ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tggtttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgcccctttc ctcgatctcg ctccccctt cggttcttcc gaccgggtcc cccctccctt 300
ttttgtttct gttttgtttt gttttgtctac gagtcacat tcctgtttgt aatccttggg 360
ttcgnccggt tttctgtttt cagtaaagtc tcgttaacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaaat ttccca 446

```

<210> 234

<211> 1891

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1891)

<223> jun d proto -oncogene (JUND) gene.

<400> 234

```

ccgaggctat aagagggcgc acaagtggcg cgccgcagga gccgcgccca gtggagggcc 60
ggcgctgctg gccgcggcgc gggcgggcgc agggccgagc ggacgggggg gcgcggggcc 120
cccgggagcg cgcgccact ccccccggg ccggcgcgcg gggggaggcg gaggatggaa 180
acacccttct acggcgatga ggcgctg agc ggccctggcg gcggcgccag tggcagcggc 240
ggcacgttcg cgtccccggg ccgcttgttc ccggggcgcg ccccgacggc cgcgcccggc 300
agcatgatga agaaggacgc gctgacgctg agcctgagt agcaggtggc ggcagcgctc 360
aagcctgcgc ccgcgccgc ctctacccc cctgcgcgc acggcgcccc cagcgcgcca 420
cccccgacg gcctgctcgc ctctcccgac ctggggctgc tgaagctggc ctcccccgag 480
ctcgagcgcc tcacatcca gtccaacggg ctggtcacca ccacgcgcag gagctcacag 540
ttcctctacc ccaaggtggc ggccagcgag gagcaggagt tcgcccaggg cttcgtcaag 600
gccctggagg atttacaaa gcagaaccag ctcggcgcgg gccgggc cgc tgccgccgcc 660
gccgcgcgc cgggggggcc ctcgggcacg gccacgggct ccgcgcccc ccggcgagctg 720

```

153/292

```
gccccggcgg cgcccgccgc cgaagcgcc gtctacgca acctgagcag ctacgcgggc 780
ggcgccgggg gcgcgggggg cgccgcgacg gtgcgccttc ctgccgaacc tgtgcccttc 840
ccgcgcggcg cacccccagg cgcgt tgggg ccgcgcggcc tggctgcgct caaggacgag 900
ccacagacgg tgcccgacgt gccgagcttc ggcgagagcc cgcggttgtc gcccatcgac 960
atggacacgc aggagcgcat caaggcggag cgcaagcggc tgcgcaaccg catcgccgcc 1020
tccaagtgcc gcaagcgcaa gctggagcgc atctcgcgcc tgggaagagaa agtgaagacc 1080
ctcaagagtc agaacacgga gctggcgctc acggcgagcc tgctgcgca gcagggtggc 1140
cagctcaagc agaaagtcc cagccacgtc aacagcggct gccagctgct gcccagcac 1200
caggtcccgg cgtactgagt cgggcatggc ggccacctc aagggcggg ctgcggggg 1260
ggtgtcgtag gcgcccggg cttggagagg gtgcggccct ccaccccccc ctcccagag 1320
gtgcccagga actcagagag gcgcggcccc ggggattccc ccccgagggtg cccaggactc 1380
ggaaggggcg ccccgactc gacaagctgg acccctgct cccggggcg agcgcatgac 1440
cccccgccc tcgcgctgcc tctttcccc gcgcggccgc cccgtgttg acaaaccgc 1500
gcgctctcgg tgcccctttg tacacgcgc cgcaaggggg ctccgaggg gcgcacgtca 1560
aaccctgcct ttcctttact tttacttttt tttttcttt ggaagagaga agaacagagt 1620
gttcgattct gccctattta tgtttctact cggggaacaa acgttggttg tgtgtgtg 1680
tgttttcttg tgttggtttt ttaaagaaat gggaagaaga aaaaaaatt ctcc gccct 1740
ttcctcgatc tcgctcccc ttcggtcttt cgaccgtccc cccctcccct tttttgttc 1800
tgttttgttt tgttttgcta cgagtccaca ttcctgtttg taatccttgg ttgcgccgt 1860
tttctgtttt cagtaaagtc tcgttacgcc a 1891
```

<210> 235

<211> 421

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(421)

<223> 3' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of
chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 235

```
acaaaaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg gagcatgagg 60
aggaaaaatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
cccggaaccc gaaacggaag ccccgtttaa tggaggagga tgagctgcc tcttgntca 240
ttaaggatga cgtgaagta gaaaggctca cctgtgaaga agaggaggag aaaatatattg 300
ggagggggtc ccgcagcgc cgtgacgtgg actacagtga cgccctcacg gagaagcagt 360
ggctaaaggg cctcgaaga cggcatttng gaggaattng aagaggaata c ggttaagaa 420
g 421
```

<210> 236

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 5' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```
tggcaatttt ctgccgggca ctcttaaaca ctgactgtaa gacgatggag tottcataga 60
totgggatcc ctccagggtg aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggtcgcc taggctccgg tacttatgat tacgaatcct ttcccttatt tttttgaaat 180
ccactggctt cctaattaat tcatagtatt ctggtaattc ttcccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgccctgaac tgtttccttc tatttccaac tgagaattac 300
tgggcacctt ctccacgtta cacctatctt tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgtcagt ttggggggga tttggtgaca gntttntcag cgggagggcg 420
gcctcttctc ttcttagg                                     438
```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin
dependent regulator of chromatin, subfamily a,
member 2 (SMARCA2) gene.

<400> 237

```
aaaaattttc tgttaccaa ttttacaact tctaataaga ctactataac tttatgtaaa 60
ctgatgaaga tgtgctgatt aacatattct gtgatatggg ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatttat cagtaaagtgt aaaatatattg aggcatttag 180
ccatacacac actagaactt tttaaaactt tgtoctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag tottcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgcc caccagggc cttcgccggg gcctgggct 360
tcccctgggc caattcttgg gctagtcca ggaccaggac catccccagg ttccgtccac 420
agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tcccacagga aggcattgat caaatgcata agcccatoga tggatatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
ctcaccagg gcatggggcc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcaccacacc catctccatt aggagcccc gagcacgtct ccagccctat gtctggagga 720
ggcccaactc cacctcagat gccaccaagc cagccggggg cctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtccc tcacctttca gtctgtcca gctgcatcag 840
cttcgagctc agatttttagc ttataaaatg ctggcccgag gccagc ccct ccccgaaacg 900
ctgcagcttg cagtccaggg gaaaaggacg ttgcctggct tgcagcaaca acagcagcag 960
caacagcagc agcagcagca gcagcagcag cagcagcagc agcaacagca gccgcagcag 1020
cagccgcccgc aaccacagac gcagcaacaa cagcagcccg cccttggttaa ctacaacaga 1080
ccatctggcc cggggccgga gc tgagcggc ccgagcacc cgcagaagct gccggtgccc 1140
gcgcccggcg gccggccctc gcccgcgccc cccgcagccg cgcagccgcc cgcggccgca 1200
gtgcccgggc cctcagtgcc gcagccggcc cgggggcagc cctcgccgt cctccagctg 1260
cagcagaagc agagccgcat cagcccccac cagaaaccgc aaggcctgga ccccgctgaa 1 320
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gaaaatctgc ctggctcttt gccaccagat ttaagaacca aagcaaccgt ggaactaaaa 1440
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agggacacga cctggagac ggctctcaac tccaaa gcat acaaaccggag caagcgccag 1560
actctgagag aagctcgcat gaccgagaag ctggagaagc agcagaagat tgagcaggag 1620
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ttaaggaat atcatcggtc tgtggccgga aagatccaga agctctccaa agcagtggca 1740
acttggcatg ccaacactga aagagagcag aagaaggaga cagagcggat tgaaaaggag 1800
agaatgccc gactgatggc tgaagatgag gagagttata gaaaactgat tgatcaaaag 1860
aaagacaggc gtttagctta ctttttgcag cagaccgatg agtatgtagc caatctgacc 1920
```

```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980
aggaagaaga aggctgagga gaatgcagag ggtggggagt ctgccctggg accggatgga 2040
gagcccatag atgagagcag ccagatgagt gacctccctg tcaaagtgac tcacacagaa 2100
accggcaagg ttctgttcgg accagaagca cccaaagcaa gtcagctgga cgcctggctg 2160
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aagcaagacg tggatgatga atacagcatg cagtacagtg ccaggggctc ccagtcctac 240 0
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ctttcgactc tatctaactg gacatatgaa tttgacaaat gggctccttc tgtggtgaag 2700
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aagctgactc aggtcttgaa cactcactat gtggcccca gaaggatcct cttgactggg 2940
accccgctgc agaataagct ccctgaactc tgggccctcc tcaacttcc cctcccaaca 3000
atttttaaga gctgcagcac atttgaacaa tggttcaatg ctccatttgc c atgactggg 3060
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gtggaatatg tgatcaagtg tgacatgtca gctctgcaga agattctgta tcgccatatg 3240
caagccaagg ggtccttct cacaga tggg tctgagaaag ataagaaggg gaaaggagg 3300
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tctgaagatc gtgctgcttt gctgaagaaa ttcaatgaac ctggatccca gtatttcatt 3660
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cgcacggggc agcagaacga ggtccgggta ctgaggctct gtaccgtgaa cagcgtggag 3840
gaaaagatcc tcgcggccgc aaaatacaag ctgaacgtgg atcagaaagt gatccaggcg 3900
ggcatgtttg acca aaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg 3960
gagcatgaag aggaaaatga ggaagaagat ggaagtaccg acgatgagac tctgaaccaa 4020
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aaaatatttg ggagggggtc ccgccagcgc cgtgacgtgg actacagtga cgcctcacg 4260
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ggcgacagc tcagtgaagt cttcattcag ttaccttcaa ggaaagaatt accagaatac 4560
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acgttcaacc tggagggatc ccagatctat gaagactcca togtottaca gtcagtgttt 4740
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gaggaagagg aagatgaaga agagtcaag tccgaggcaa aatcagtcaa ggtgaaaatt 4860
aagctcaata aaaaagatga caaaggccgg gacaaaggga aaggcaagaa aaggccaaat 4920
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agaactgaat ccttccctcc cctgtctcat ttctaccag tgagttcatt tgtcatatag 5100
gcactgggtt gtttctatat catcatcgtc tataaactag ctttaggata gtgccagaca 5160
aacatatgat atcatggtgt aaaaaacaca cacatacaca aatatttgtg accaa atggg 5220
cctcaaagat tcagattgaa acaaacaaaa agctttt 5257

```

<210> 238

<211> 507

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma
isoform (PPP2R2C) gene.

<400> 238

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tacatgctca cccgggacta ccttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccaggt ccatgactac cttcggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgacggaa caccaagcgg gacgtgacct 240
tgggagccct cgagggaaaag cagcaagccc cgggctgtgc tcaagccacg gcgcgtgtgc 300
gtgggggggc aagcgccggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcacccggc tgaggaacat catttgccat tcgcccgcac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatttt tgacattgca ttaggtattn 480
tgcaatttcc cggnccttgc caacca                                     507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma a
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaca attactgcca aacacaattc tggcctagga aagcgggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tctcatcag tgggtgtgact 120
ttcttcccct ccttgcatcg cggtcgtgaa ggtcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggccgggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca gggtgttggg ggcggcgatg gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggg gaagtccaag ctgttccaaa atgatgtcat cacgccggcc 360
cttgcccccc acgnaaangg ncnnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctnagnagcn tncaggntca agtnccnttt ggtnttnccc gatogaacat ncggaagaat 480
tttttttagg ccccntcat gatgaacgtg tncgttccct t                                     521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3
(THBS3) gene.

<400> 240

```
cagattcatt nnngganntg cctgtgacaa ttgccccaac gttcccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatgggtgc 120
aggcctgggg ctgaaggggt ggctggggga cctgtgagaa tttggatcag gtggggatga 180
agcagggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

```
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gccagtcagg atctgcaggT aattgacctg ctgactgttg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctcaactgctg gggacatcta cctcttatcc 180
accttcgcgc tgccccccaa gcagggtggt gtccctctttg g cctctattc tcgccaagac 240
aacactcgat ggctggaggc ctctgttgta ggcaagatca acaaagtact ggtgcgatac 300
cagcgggagg atggcaaaagt ccacgcctgT aacctacagc aagcgggcct ggctgatggg 360
cgcacacaca cagttctcct gcgactccga ggtccctcca gaccagccc tgccctacat 420
ctctacgttg actgcaaact gggtgaccaA catgcaggcc ttccagcact ggccccatt 480
cctccagcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggctttg tggaatctat gaaaattatt ctgggtgggt ccatggcccg ggtaggagcc 600
ctgagtgagt gtccattcca aggggaocag tccatccaca gtgcagtgc caatgcactg 6 60
cactccattc taggggagca gaccaaggcg ctggtcacc aactcaccct cttcaaccag 720
atcctggttg agctgcggga tgatatacga gaccaggtaa aggaaatgtc cctgatccga 780
aacaccatta tggagtgtca ggtgtgcggc ttccatgagc agcgttccca ctgcagcccc 840
aatccctgct tccgaggtgt ggactgcagt gaagtgtacg agtaccagc ctaccgctgt 900
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gctcacgctg acccctgttt cccgggctcc agctgcacA acaccatgcc cggcttccac 1020
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gcctgtgaca acgacgtgga tggggatggc atccccaatg gattggacaa ttgccctaaa 1740
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cagctgccccA atagctcca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
ggggatgatg acaatgatgg catcccagat tatgtgcctc ctgggtcccg taactgcgcg 2040
```


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```

ctgggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggtcgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg ggcctatcag accgtcgccc tggatcctga gggatgatgct 2220
cagattgacc caaactgggt tgtgctcaac cagggcatgg aaatcgttca gaccatgaac 2280
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gtggcggatt ctgggggtgat cattgacaca tccatgcgag gggggcgctc tgggtgtattc 2760
tgcttctccc aagaaaacat aatttggctc aatctccagt atcgatgcaa tgacacagtg 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaagggtgtg a 2871

```

<210> 242

<211> 509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1) gene.

<400> 242

```

cacttttatt ttnccttaca caatgacgtg ttgctggggc ctaatgtncct cacataaacag 60
tagaaaaacca aaatttgttg tcatctcttc aaagantcga ganttgcgta caaaaaaac 120
cttacataaan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccacggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
cctacggctt gggactttcc aaccctggac aggaccgca aggncaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccgaac actcaggccc tggacangtt taataaccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggctgggtt cnggttacag gtttcagggg cattttnttt tcggaggggt tnttcccggt 480
tcgtgagggg aggctgaggg tttntgctt 509

```

<210> 243

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1) gene.

<400> 243

```

gatcaccgcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
tactcgggtg ggatcgggtg ctccatcctg gcctcactgt ccaccttcc a gcagatgtgg 120
attagcaagc aggagtacga cgagtcgggc ccctccatcg tccacggcaa atgtttctaa 180
acggactcag cagatgcgta gattttgctg catgggttaa ttgagaatag aaatttgccc 240

```

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```

ctgggaaatt gcacacacct catgctagcc tcacgaaact gggaataagc ctttcgaaaa 300
gaaattgtcc ttgaagcttg tatctgg tat cagcactggg ntgtaggaa nttgttgctg 360
atttttgacc ttgtanttgga agtttaactg ttt                                     393

```

<210> 244

<211> 1919

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1919)

<223> actin, gamma 1 (ACTG1) gene.

<400> 244

```

gtctcagtcg ccgctgccag ctctcgcact ctgttcttcc gccgctccgc cgtcgcgttt 60
ctctgccggt cgcaatggaa gaagagatcg ccgctctggt cattgacaat ggctccggca 120
tgtgcaaaagc tggttttgct ggggacgacg ctccccgagc cgtgttttcc t tccatcgtcg 180
ggcgccccag acaccagggc gtcatggttg gcatgggcca gaaggactcc tacgtgggcg 240
acgaggccca gagcaagcgt ggcacctga cctgaagta cccattgag catggcatcg 300
tcaccaactg ggacgacatg gagaagatct ggcaccacac cttctacaac gagctgcgcg 360
tggccccgga ggagcaccga gtgctgc tga ccgaggcccc cctgaacccc aaggccaaca 420
gagagaagat gactcagatt atgtttgaga ccttcaaac cccggccatg tacgtggcca 480
tccaggccgt gctgtccctc tacgcctctg ggcgcaccac tggcattgtc atggactctg 540
gagacggggg caccacacg gtgcccctc acgagggcta cgccctcccc cagcccatcc 600
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cggtttgcac ttacgcctgt aaatgtattc attcttaatt tatgtaagg t tttttttgta 1800
cgcaattctc gattctttga agagatgaca acaaattttg gttttctact gttatgtgag 1860
aacattaggc ccagcaaca cgtcattgtg taaggaaaaa taaaagtgt g cgtgaacc 1919

```

<210> 245

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<220>
<221> misc_feature
<222> (1)..(467)
<223> 3' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 245
ccgccgcgcg gcagctgtgc ttgctctacc tgtcggcggg gctcctgtcc cggctcggcg 60
cacttncaac ttggacactc gggaggacaa cgtgatccgg aaatatggag accccgggag 120
cctcttcggc ttctcgctgg ccatgcaact gcaactgcag cccgaggaca agcggctgtt 180
gctcgtgggg gccccgcggg agnaagcgct tccactgcag agagccaac a gaacgggagg 240
gctgtacagc ttgcgacatc accgcccggg ggccatgcac ggggatcgag tttnataacg 300
atgcttgacc ccacgtcaga aagcaaggaa gattagttgg atnggggggc aacgtccaga 360
gccaaaggtc agggggcaag gtcgtgacat gtgttnaccc tattgaaaaa aggcagcatt 420
ttattacgna gcangatttc cgagaca ttt ttgggcgttt tttttcc 467

<210> 246
<211> 473
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(473)
<223> 5' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 246
gccctctccc atccatatcg tcttcaatcc tgagattctg actcaggaca naacaccgcc 60
caaagatgtc tcgggattcc tgcttcgtat taacatgctg ccttttttca tatcgggtgag 120
cacatgtcac gaccttgccc cctggacctt ggctctggac ggtgacccc atccactgat 180
cttccttgct ttctgacgtg gggtc agcat cgttatcaaa ctcgatccgc gtgcattggc 240
ccggggcggg ggatgtcgca gctgtacagc cctcccggtc tgttggtct ctgcagtggg 300
aagcgcttct gccccgcggg cccccacgga gcaacagccg cttgtcctcg ggctgcagtt 360
gccagtgcag gggccagcga gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420
gatcaagttg ttcctnccga gttttccaag tttgaagggt tgcgcaaggc cgt 473

<210> 247
<211> 5611
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5611)
<223> integrin, alpha 6 (IT GA6) gene.

<400> 247
gcgcgaccgt cccgggggtg gggccgggag cagcggcgag aggaggcgaa ggtggctgcg 60
gtagcagcag cgcggcagcc tcggaccag cccggagcgc agggcgggcc ctgcagggtc 120
ccgctcccc ccccggtgct cgcgccatgg ccgcgcggg gcagctgtgc ttgctctacc 180
tgtcggcggg gctcctgtcc cg gctcggcg cagccttcaa cttggacact cgggaggaca 240
acgtgatccg gaaatatgga gaccccgga gcctcttcgg cttctcgctg gccatgcact 300

```

ggcaactgca gcccaggagc aagcggctgt tgcctcgtggg ggccccgcgc ggagaagcgc 360
ttccactgca gagagccaac agaacgggag ggctgtacag ctgcgacatc accgccccgg 420
ggccatgcac gcggatcgag ttgtataacg atgctgaccc cagctcagaa agcaaggaa 480
atcagtgatg gggggtcacc gtccagagcc aagggtccagg gggcaaggtc gtgacatgtg 540
ctcaccgata tgaaaaaagg cagcatgtta atacgaagca ggaatcccga gacatctttg 600
ggcgggtgta tgcctcgtagt cagaatctca ggattgaaga cg atatggat gggggagatt 660
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actggaaagg gattgttcgt gtagagcaaa agaataacac tttttttgac atgaacatct 840
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ttcctgctaa cagttactta ggtttttctt tggactcagg gaaaggatatt gtttctaaag 960
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gctctcgtag gcgagtgaat tcac ttccag aagttcttcc aattctgaat tcagatgaac 1980
ccaagacagc tcataattgat gttcacttct taaaagaggg atgtggagac gacaatgtat 2040
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gcgatgacgc ccatgaggct aaactgattg caacgtttcc agacacttta acctattctg 2280
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tgtagattg ctgattgct aaggagctga tacttgacag ttttttagac ctgtgttact 5280
aaaaaaaaaga tgaatgtcgg aaaaggggtg tgggaggggtg gtcaacaaag aaacaaagat 5340
gttatgggtg ttagacttat ggttggttaa aatgtcatct caagtcaagt cactgggtctg 5400
tttgcatthg atacattttt gtactaacta gcattgtaaa attatttcat gattagaaat 5460
tacctgtgga tatttgtata aaagtgtgaa ataaaatttt tataaaagtg ttcattgttt 5520
cgtaacacag cattgtatat gtgaagcaaa ctctaaaatt ataaatgaca acctgaatta 5580
tctatttcat caaaaaaaaa aaaaaaaaaa a 5611

```

<210> 248

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)
homolog (RAD9) gene.

<400> 248

```

cctttattca agagaccaga tgggttgccc caggatccgg ctgccagacc ctgaggccaa 60
gcacggntgg agaccacagn acctgggcct gccnttgccc tgagctgcag cctcggcccc 120
aggatcctgn tcacagntca ccgcaggnc gngncaggaa gcagccctgg gggantggaa 180
cgntgctatt gattcattaa aaaaagaaaa gaaan taca ccaaggttcc atnttccccg 240
tgacaggtgg gcctnagggg tcggggtnac ccccccccag natggcagca tgatttntnt 300
acaatcaatc catcatntgg ggcacagggt gggtttcggg ggctatttnt tggctttggc 360
gaaattncgg gntggggtaa tgggtnggcc tccagggtta aggcca 406

```

<210> 249

<211> 2102

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2102)
<223> rad9 (s. pombe) homolog (RAD9) gene.

<400> 249
gcgcgggaag ggaccccgga cccggaggtc gcggagagct gggcagtgtt ggccgctggc 60
ggagcgctgg ggagcatga agtgccctgt cacgggcggc aacgtgaagg tgctcgga 120
ggccgtccac tccctgtccc gcatcggga cgagctctac ctggaaccct tggaggacgg 180
gctctccctc cggacggtga actcctcccg ctctgcctat gcctgctttc tctttgcccc 240
gctcttcttc cagcaatacc aggcagcca c ccctggtcag gacctgctgc gctgtaagat 300
cctgatgaag tctttcctgt ctgtcttccg ctactggcg atgctggaga agacggtgga 360
aaaatgctgc atctccctga atggccggag cagccgcctg gtggctccagc tgcattgcaa 420
gttcggggtg cggaagactc acaacctgtc cttccaggac tgtgagtccc tgcaggccgt 480
cttcgaccca gcctcgtgcc cccacatgct cgcgcgcccc gacgggttc tgggggaggc 540
tgttctgccc ttctctcctg cactggctga agtgacgctg ggcattggcc gtggccgcag 600
ggatcatcctg cgcagctacc acgaggagga ggcagacagc actgccaag coactggtgac 660
tgagatgtgc cttggagagg aggatttcca gcagctgcag gccaggaa g ggggtggccat 720
cactttctgc ctcaaggaat tccgggggct cctgagcttt gcagagtcag caaacttgaa 780
tcttagcatt catthttgatg ctccaggcag gcccgccatc ttcaccatca aggactcttt 840
gctggacggc cactttgtct tggccacact ctccagacacc gactcgcact cccaggacct 900
gggctcccca gagcgtcacc agccagt gcc tcagctccag gctcacagca caccacacc 960
ggacgacttt gccaatgacg acattgactc ttacatgac gccatggaaa ccactatagg 1020
caatgagggc tcgcggtgct tgccctccat ttccctttca cctggcccc agcccccaa 1080
gagccccgt cccactccg aggaggaaga tgaggctgag ccagtagac tgccctgggac 1140
tccccaccc aagaagttcc gctcactgtt cttcggtcc atcctggccc ctgtacgctc 1200
ccccagggc cccagccctg tgctggcgga agacagttag ggtgaaggct gaaccaagaa 1260
cctgaagcct gtaccagag gccttgact agacgaagcc ccagccagtg gcagaactgg 1320
gtctctcagc cctggggatc agaaaggtgg gcttgctgga g ctgagctgt ttcactgcct 1380
ctcgaggcc ccagctggct gtcactgtaa agctgtccca cagcggtcgg gcctgggccc 1440
ttatctcccc acaaccccc gccaatcagg actttccaga cttggccctg aactactgac 1500
gttctacct cttattttctc attgagcctc aggctatact ccagctggcc aaggctggaa 1560
acctgtctcc ctccaggctca ccttcctaag gaaaatgtca tagtaggtgc tgctggcccc 1620
tggtgatcca gttctctgc caatcatgac ctgttccttc ctgaagtcct gggcatgcat 1680
ctgggacccc cgtggagctg acaagttttc cttgctttcc tgatactctt tggcgctgac 1740
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gtgccgagac tcccaagcgg ctctgtgcag aagagctgcc aggcagtgtc ttagatgtga 1860
gacggaggcc atggcgagaa tccagctttg acctttatc aagagaccag atgggttgcc 1920
ccaggatccg gctgccagcc ctgaggccaa gcacggctgg agaccacga cctggcctgc 1980
cgttgccctg agctgcagcc tcggccccag gatcctgctc acagtcaccg cagggtgcagg 2040
caggaagcag ccctggggga ctggacgctg ctattgattc attaaaaaaa gaaaagaaaa 2100
at 2102

<210> 250
<211> 365
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(365)
<223> 3' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 250
tccaatatatt attattctga caggtttaga atactaggat aaataagtaa tatttntct 60

164/292

```

tacagaaaat tgtaatgata ccattgagta caattaaaca ctctgagaat ttcacagaaa 120
catcagaatt ttaatagaca gtagccagcg tccttgtggc cagtgtgagt gacttctcac 180
agctgcaaac accctgggcc agatttctta aaacagctac atgacaaaaa caatgctatt 240
gacatccaat aatgctaaag cctgggtacc acccgggtcc cactgactgt ggn ttccaaa 300
catctctcca ctgactgtgg ntttcaaccn caaggnaagg gaaatgggat attccttggg 360
ctctt                                     365

```

<210> 251

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 251

```

cgtggctacc attgtcactc gtaggggatg tggagtgaga acagcattta gtgaagttgt 60
gcaacggcca gggttgtgct ttctagcaaa tatgctgt ta tgtccagaaa ttgtgtgtgc 120
aagaaaaacta ggcaatgtac tcttccgatg tttgtgtcac acaacactga tgtgactttt 180
atatgctttt tctcagatct ggtttctaag agttttggcg cgggcggggc tgtcaccacg 240
tgcagtatct caagatatcc aggtggggcca gaagagcttg tcagcaagag ggagggacag 300
aattctccca ggcgtt aaca caaaatccat ggggcagtat ggatgggcag gtcntctgt 360
tggcaaacctc agttcccaag tcacagggaa gganaggcag gaaagtttca actttcccaa 420
agggtttagg ggcttttcca cttcaatgtc tta                                     453

```

<210> 252

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> activating transcription factor 3 (ATF3)
gene.

<400> 252

```

gcagccaggc ggcactgca cagctctctt ctctcgccgc cgcccagagc caccottcag 60
cccgcgcgcc ggccg tgagt cctcggtgct cgcccgcggg ccagacaaac agcccgcggc 120
accgcgtccc gaccctggcc gcccagagcg gagcctggag caaaatgatg cttcaacacc 180
caggccagggt ctctgcctcg gaagtgaagt cttctgccat cgtcccctgc ctgtcccctc 240
ctgggtcact ggtgtttgag gattttgcta acctgaagcc ctttgtcaag gaagagc tga 300
ggtttgccat ccagaacaag cacctctgcc accggatgtc ctctgcgctg gaatcagtca 360
ctgtcagcga cagaccctc ggggtgtcca tcacaaaagc cgaggtagcc cctgaagaag 420
atgaaaggaa aaagaggcga cgagaaagaa ataagattgc agctgcaaag tgccgaaaca 480
agaagaagga gaagacggag tgccctgcagc ttcag tatta gcagagccac aggcgcgctc 540
tgtggcatca ccagggtttc tctgaagaag aggggtctgca ttttcctaaa cccagtgtcg 600
ctctcccctc tcccctcttc ctctcgagc ttgatgagcc ccggtgtgtc ccaggagtcg 660
gagaagctgg aaagtgtgaa tgctgaactg aaggctcaga ttgaggagct caagaacgag 720
aagcagcatt tga tatacat gctcaacctt catcggccca cgtgtattgt ccgggctcag 780

```

165/292

```

aatgggagga ctccagaaga tgagagaaac ctctttatcc aacagataaa agaaggaaca 840
ttgcagagct aagcagtcgt ggtatggggg cgactgggga gtccctcattg aatccctatt 900
ttatacccaa aaccctgaag ccattggaga gctgtcttcc tgtgtacctc tagaa tccca 960
gcagcagaga accatcaagg cgggagggcc tgcagtgatt cagcaggccc ttcccattct 1020
gccccagagt gggctcttga ccagggaag tgcatctttg cctcaactcc aggatttagg 1080
ccttaacaca ctggccattc ttatgttcca gatggcccc agctgggtgtc ctgcccgcct 1140
ttcatctgga ttctacaaaa aaccaggatg cccaccgtta gattcaggca gcagtgtctg 1200
tacctcgggt gggagggatg gggccatctc cttcaccgtg gctaccattg tccctcgtag 1260
gggatgtgga gtgagaacag ctttagtga agttgtgcaa cggccagggt tgtgtcttct 1320
agcaaatatg ctgttatgtc cagaaattgt gtgtgcaaga aaactaggca atgtactctt 1380
ccgatgtttg tgtcacacaa cactgatgtg acttttata gctttttctc agatctggtt 1440
tctaagagtt ttggggggcg gggctgtcac cacgtgcagt atctcaagat attcagggtg 1500
ccagaagagc ttgtcagcaa gaggaggaac agaattctcc cagcgtaaac acaaaatcca 1560
tgggcagcat gatggcagg cctctgttgc aaactcagtt ccaa agtcac aggaagaaa 1620
cagaaagtcc aacttccaaa gggtaggac tctccactca atgtcttagg tcaggagttg 1680
tgtctaggct ggaagagcca aagaaatatt ccattttcct ttccctgttg ttgaaaccac 1740
agtcagtgga gagatgtttg gaacacagtc agtggagctg gtggtaccag gtttagcatt 1800
attggatgtc aaaagcattt tttttgtcat gtagctgttt taagaaatct ggcccagggt 1860
gtttgcagct gtgagaagtc actcacactg gccacaagga cgctggctac tgtctattaa 1920
aattctgatg tttctgtgaa attctcagag tgtttaattg tactcaatgg tatcattaca 1980
attttctgta agagaaaata ttacttattt atoctagtat tccaaacctg tcagaata at 2040
aaatattgtg gtaaaa 2056

```

<210> 253

<211> 502

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma
viral oncogene homolog 2 (AKT2) gene.

<400> 253

```

acatcatctc gtacatgacc acaccagcc cantacnntt tccacggccc ggccatagtc 60
attgtcctcc agcacctcag gcgccaggta ctccgggggc ccacagaagg ttttcatggt 120
ggccccgtca ctgatgccct ctttgcagag gccaaagtca gtgatcttga tgtggccatc 180
tttgtccagc atgaggtttt ccagcttgat gtgcgggtat accacgtccc gcgagtgcaa 240
gtactcaaga gccgagacaa tctctgcacc ataaaaccgg gcccgctcct ctgtgaagac 300
acgctcccgg ggacaggtag gaagaacagc tcacccccgt tgggcatact ccattcacia 360
aggcacaggg cgggtcgttg ggtctgggaa gggcattant ttcaggcggc agttgaggga 420
acgggggttg nggggtgttt ctgggaggga cccgggtttt cggttgattn ttttgaggcg 480
attttcatcc nttgggcaat tt 502

```

<210> 254

<211> 1715

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog
2 (AKT2) gene.

<400> 254

```

gaattccagc ggcggcgccg ttgccgctgc cgggaaacac aaggaaaggg aaccagcgc a 60
gcgtggcgat gggcgggggt agagccccgc cggagaggct gggcggtgc cggtagacaga 120
ctgtgccctg tccacgggtgc ctctgcatg tcctgctgcc ctgagctgtc ccgagctagg 180
tgacagcgta ccacgctgcc accatgaatg aggtgtctgt catcaaagaa ggctggctcc 240
acaagcgtgg tgaatacatc aagacctgga ggccacgg ta ctctctgctg aagagcgacg 300
gctccttcat tgggtacaag gagaggcccg agggccctga tcagactcta ccccccttaa 360
acaacttctc cgtagcagaa tgccagctga tgaagaccga gaggccgcga cccaacacct 420
ttgtcatacg ctgcctgcag tggaccacag tcatcgagag gaccttccac gtggattctc 480
cagacgagag ggagga gtgg atgcggggcca tccagatggt cgccaacagc ctcaagcagc 540
gggccccagg cgaggacccc atggactaca agtgtggctc cccagtgac tcctccacga 600
ctgaggagat ggaagtggcg gtcagcaagg cacgggctaa agtgacctg aatgacttcg 660
actatctcaa actccttggc aagggaacct ttggcaaagt catcctgggt cgggagaa gg 720
ccactggccg ctactacgcc atgaagatcc tgcgaaagga agtcatcatt gccaaggatg 780
aagtgcgtca cacagtcacc gagagccggg tcctccagaa caccaggcac ccgttcctca 840
ctgcgctgaa gtatgccttc cagaccacag accgcctgtg ctttgtgatg gagtatgcc 900
acgggggtga gctgttcttc cacctgtccc gggagc gtgt cttcacagag gagcggggccc 960
ggttttatgg tgcagagatt gtctcggctc ttgagtactt gcactgcgg gacgtgggtat 1020
accgcgacat caagctggaa aacctcatgc tggacaaaga tggccacatc aagatcactg 1080
actttggcct ctgcaaagag ggcacagtg acggggccac catgaaaacc ttctgtggga 1140
ccccggagta cctggcgccct gaggtgctgg aggacaatga ctatggccgg gccgtggact 1200
ggtgggggct ggggtgtggtc atgtacgaga tgatgtgcgg ccgcctgcc ttctacaacc 1260
aggaccacga gcgcctcttc gagctcatcc tcatggaaga gatcgccttc ccgcgcacgc 1320
tcagccccga ggccaagtcc ctgcttgctg ggctgcttaa gaaggacccc aagcagaggc 1380
ttggtggggg gccacgcgat gccaaaggag tcatggagca caggttcttc ctcagcatca 1440
actggcagga cgtggtccag aagaagctcc tgccacctt caaacctcag gtcacgtccg 1500
aggtcgacac aaggtacttc gatgatgaat ttacgcgcca gtccatcaca atcaccccc 1560
ctgaccgcta tgacagcctg ggctt actgg agctggacca gcggacccac ttccccagt 1620
tctcctactc ggccagcatc cgcgagttag cagtctgcc acgcagagga cgcacgctcg 1680
ctgccatcac cgctgggtgg ttttttacc ctgcc 1715

```

<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding
protein, beta (neural) (S100B) gene.

<400> 255

```

gagagatgt ctgagctgga gaaggccatg gtggcctcat cgacgttttc caccaatatt 60
ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcataca 120
atgagctttc ccatttctta gaggaatca aagagcagga ggttgtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccatggtta ctactgcctg ccacgagttc tttgaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggacgggt catggcaaga naggcaggac aggcaagggg 360
tttgacggct tagttaggga gcttgagggt tttccagcog tntttnttg gttaatttag 420
ggaaggttg a 431

```

<210> 256

<211> 1095
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1095)
 <223> s100 calcium-binding protein, beta (neural)
 (S100B) gene.

<400> 256
 tgccgcccag gacccgcagc agagacg acg cctgcagcaa ggagaccagg aaggggtgag 60
 acaaggaaga ggatgtctga gctggagaag gccatggtgg ccctcatcga cgttttccac 120
 caatattctg gaaggaggag agacaagcac aagctgaaga aatccgaact caaggagctc 180
 atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggagggt tgtggacaaa 240
 gtcattgaaa cactggacaa tgatggagac ggcgaatgtg acttccagga attcatggcc 300
 tttgttgcca tggttactac tgcctgccac gagttctttg aacatgagtg agattagaaa 360
 gcagccaaac ctttctctgta acagagacgg tcatgcaaga aagcagacag caagggtctg 420
 cagcctagta ggagctgagc tttccagccg tgtttagact aattagga ag cttgatttgc 480
 tttgtgattg aaaaattgaa aacctctttc caaaggctgt tttaacggcc tgcattcatc 540
 tttctgctat attaggcctg tgtgtaagct gactggcccc agggactctt gttaacagta 600
 acttaggagt cagggtctcag tgataaagcg tgcaccgtgc agcccgccat ggccgtgtag 660
 accctaaccg ggagggaacc ctgact acag aaattacccc ggggcaccct taaaacttcc 720
 actaccttta aaaaacaaag ccttatccag cattatttga aaacactgct gttcttttaa 780
 tgcgttcctc atccatgcag ataacagctg gttggccggt gtggccctgc aagggcgtgg 840
 tggcttcggc ctgcttcccg ggatgcccct gatcaccagg tgaacgctca gcgctggcag 900
 cgtcctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960
 cgtggcctcc gtgacctatg cgattcaagt cgcggtgca ggatccttgc ctccaacgtg 1020
 cctccagcac atgcggcttc cgagggcact accgggggct ctgagccacc gcgagggcct 1080
 gcgttcaata aaaag 1095

<210> 257
 <211> 542
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(542)
 <223> 3' terminal sequence. atp-binding cassette,
 sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257
 ttttaaaatc tactttaatt ctgttataaa atttataatg cagtttaaac tatgatttct 60
 ctccacttga tgatgtctct cactctgttc ctttaattac gaagtctctg aagactctga 120
 acttgactga ggaaatgtta aacagatacc tcttcataat tctgtaagt tttgctttta 180
 actttgaata aatgtcatat ctaaacaaat attaaaaagt atttaacatc tcatacagtc 240
 agagttcact ggccgtttgt tccagcctgg acactgacca ttgaaaaata gatgcctttc 300
 tgtgccagca gctgctgatg cgtgccatgc tccttgactc tgccattctg aaacaccact 360
 attaatgtct cattctggat ggtggacagg cggtagcaa tcacaatgca ggtgcggcct 420
 tctctggcta tgccagggct tcttgacaaa cttttcacc tactgtatcc agagctgacg 480
 tggctcatcc aaaagcaaaa tantgggctg tctaacaagg gcacgagcta ttgccatgcg 540
 tt 542

<210> 258
<211> 4643
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4643)
<223> atp-binding cassette, sub-family b
(mdr/tap), member 1 (ABCB1) gene.

<400> 258
cctactctat tcagatattc tccagatt cc taaagattag agatcatttc tcattctcct 60
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120
tcctcctgga aattcaacct gtttcgcagt ttctcgagga atcagcattc agtcaatccg 180
ggccgggagc agtcatctgt ggtgaggctg attggctggg caggaacagc gccggggcgt 240
gggctgagca cagcgcttcg ctctctttgc cacaggaagc ctgagctcat tcgagtagcg 300
gctcttccaa gctcaaagaa gcagaggccg ctggttcgtt ccttttaggtc tttccactaa 360
agtcggagta tcttcttcca agatttcacg tcttggtggc cgttccaagg agcgcgaggt 420
cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaac t tttttaact 480
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540
gtttcgctat tcaaattggc ttgacaagtt gtatatgggt gtgggaactt tggctgccat 600
catccatggg gctggacttc ctctcatgat gctgggtgtt ggagaaatga cagatatctt 660
tgcaaatgca ggaaatttag aagatct gat gtcaaacatc actaatagaa gtgatatcaa 720
tgatacaggg ttcttcatga atctggagga agacatgacc aggtatgcct attattacag 780
tggaattggg gctgggggtg tggttgctgc ttacattcag gtttcatttt ggtgcctggc 840
agctggaaga caaatacaca aaattagaaa acagtttttt catgctataa tgcgacagga 900
gatagctgg tttgatgtgc acgatgttgg ggagcttaac acccgactta cagatgatgt 960
ctccaagatt aatgaaggaa ttggtgacaa aattggaatg ttctttcagt caatggcaac 1020
atttttctact gggtttatag taggatttac acgtggttgg aagctaacco ttgtgatttt 1080
ggccatcagt cctgttcttg gactgtcagc tgctgtctgg gcaaa gatac tatcttcatt 1140
tactgataaa gaactcttag cgtatgcaaa agctggagca gtagctgaag aggtcttggc 1200
agcaattaga actgtgattg catttgaggg acaaaagaaa gaacttgaaa ggtacaacaa 1260
aaatttagaa gaagctaaaa gaattgggat aaagaaagct attacagcca atatttctat 1320
aggtgctgct ttctgtctga tctatgcac tttatgctctg gccttctggt atgggaccac 1380
cttggtcttc tcaggggaat attctatttg acaagtactc actgtatttt ctgtattaat 1440
tggggctttt agtgttggac aggcattctc aagcattgaa gcatttgcaa atgcaagagg 1500
agcagcttat gaaatcttca agataattga taataagcca agtattgaca gctatttca a 1560
gagtgggcac aaaccagata atattaaggg aaatttggaa ttcagaaatg ttcacttcag 1620
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<210> 259

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(486)

<223> 3' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 259

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tttttc 486

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<210> 260
<211> 478
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(478)
<223> 5' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260
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tctcaggatc aagaaagtgt tggctaata agggaaagga tattttcttc caagcaaagg 180
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ttcgacagct gattacacag ttcctgtcat aaggaatgaa taattaatta tccagagttt 360
agaggaaaaa aatgactaaa aatattatta acttaaaaaa tggacagggtg ttggatgccc 420
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<210> 261
<211> 3834
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3834)
<223> selectin e (endothelial adhesion molecule 1)
(SELE) gene.

<400> 261
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ttgcttcaca gtttctctca gctctcactt tgggtgcttc cattaaagag agtggagcct 180
ggtcttacaa cacctccacg gaa gctatga cttatgatga ggccagtgc tttgttcagc 240
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tgggcatgtg gaatgatgag aggtgcagca agaagaagct tgccctatgc tacacagctg 540
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<210> 262

<211> 267

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(267)

<223> 3' terminal sequence. epidermal growth factor (beta-uromastrone) (EGF) gene.

<400> 262

gtttatgttt ttggtgattt tatttaaata attagaagaa attcatcggt gt ctataatg 60

172/292

```

aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
aatcacacca agagggaata ttctgtaggg gaaaaggaca gtaatgacta agaaactccg 180
aagcctcctg tgtaatatct taaaatanaa tgttttcatt caaatatctt aaaaaataag 240
natctaactc gaaaaaatca gtttcta                                267

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<210> 263

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 5' terminal sequence. protein kinase c
substrate 80 k-h (PRKCSH) gene.

<400> 263

```

ggagtcaggag gtgcaggggg agcagcccaa gccggccagc cctgctgagn gaagacaaaa 60
tnccgcccta cgacgagcag acgcaggcct tcacgatgac tgcccaggag gcccgcaaca 120
agttcgagga ggccgagcgg tcgctgaagg acatggagga gtccatcagg aacctggnag 180
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tacgagctca ccaccaacga atacgtctac cgccctctncc ccttcaagct tgtnttcgna 300
gaaaccctaaa ctcggggggt ctcccaccag ccttggcacc tggggggcttc atgggattgg 360
gcccgacca cnacaatttc agt                                383

```

<210> 264

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)
gene.

<400> 264

```

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cgtgaagaca cagcgcactt ccccgctgta ggcttctccc acagaacccg tttcggggcct 120
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atgtgatccc ccacc 2056

```

<210> 265

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. diphtheria toxin
receptor (heparin-binding epidermal growth
factor-like growth factor) (DTR) gene.

<400> 265

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gtcagagtgc cactgcggga ntctgtatgg tcaggatgta ggggttaact tggtcagagc 120
cactctatga gttggacttc agtcttgcc aggcgatttt gtctaccatt tgtgttttga 180
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tgccaagtct cagaagagg tgggctt cca tgctgtagc tttctgggtc cctcaccccc 300
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aactcctgnc attcttctg 379

```

<210> 266

<211> 2360

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2360)

<223> diphtheria toxin receptor (heparin-binding
epidermal growth factor-like growth factor) (DTR)
gene.

<400> 266

```

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ataaaaaaaaa aaaaaaaaaa 2360

```

<210> 267

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. integrin, beta 2
 (antigen cd18 (p95), lymphocyte
 function-associated antigen 1; macrophage antigen
 1 (mac-1) beta subunit) (ITGB2) gene.

<400> 267

```

aggagtgcgc cggtgcccc tcaccctgtg gcaagtacat ctctgcgc gagtgctga 60

```

```

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tgctgatcgg cattctcctg ctggtcattc gggaaggctc tgatccacct gacgcacctc 360
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ccctttttca agagc 435

```

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),
lymphocyte function-associated antigen 1;
macrophage antigen 1 (mac-1) beta subunit) (ITGB2)
gene.

<400> 268

```

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ctcgggtgcg tcctctctca ggagtgcacg aagttcaagg tcagcagctg ccgggaatgc 180
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cctgactcca ttgctgcca caccgggcca cagc tgctca tgaggggctg tgcggctgac 300
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ctgccgttcg tgaacacgca ccctgataag ctgcgaaacc catgccccaa caaggagaaa 660
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176/292

```

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aaaataaaac ttcaat 2776

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<210> 269

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)
homolog 1 (NEO1) gene.

<400> 269

```

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ggagaccaca aggtgtttg gaaggattnc gagagtaggt attgaaccag ntgaggttga 360
ncaaagagtt gggccatngg gggagggatt aattgaangg gaccttaaac gttttttnac 420
aacagcttga cggactttta acgggggggc 449

```

<210> 270

<211> 5297

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5297)

<223> neogenin (chicken) homolog 1 (NEO1) gene.

<400> 270

```

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cggctgaggc gcgcgggagg gaaggaggca agggctccgc ggcgctgtcg cgctgccgct 120
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gcattccaaa cacaataa ac ctgatgaagg ttattatcag tgtgtggcca ctgttgagag 540
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```

<210> 271

<211> 389

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,
transcription factor 2 (POU2F2) gene.

<400> 271

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cccacccttc aaaggggaaa agagggagga acaggggatg aaaagtintc cgcagccttc 240
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<210> 272

<211> 2048

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2048)

<223> pou domain, class 2, transcription factor 2
(POU2F2) gene.

<400> 272

179/292

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cactccagca tgggggctcc agaaataaga atgtctaagc ccctggaggc cgagaagcaa 120
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<210> 273

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 3' terminal sequence. baculoviral iap
repeat-containing 4 (BIRC4) gene.

<400> 273

```

ttttctatct ttccaccagc atggaaca at tgattccttt ttcacacaaa acaattatg 60
tgattgggga gattaactct aatctccaca tttatataca gaaagctcca tttgttaagc 120
ctatctgaaa agaataaaaa atccagatga ttaattcact tacacttaga aattaaatca 180
gtatactatg aatacacatt gtgttcagtt atagtatgat gcttcttatt cttagtctat 240
ggtttcaatt aaataacagt aaaaaaatg gataatacag ctaataccct gaaaaatcaa 300
gaaattcaaa gattatattg ccaactaaaa cactgccatg tacatttttt ttccactctg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
aatcagggta ataagaacaa cataacatgc ctaccataga gttagatta a ga 472

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<210> 274
 <211> 2540
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2540)
 <223> baculoviral iap repeat -containing 4 (BIRC4)
 gene.

<400> 274
 gaaaagggtgg acaagtccta ttttcaagag aagatgactt ttaacagttt tgaaggatct 60
 aaaacttgtg tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
 ttaaaaaactt ttgctaattt tccaagtggt agtcctgttt cagcatcaac actggcacga 180
 gcagggtttt tttatactgg tgaaggagat accgtgcggt gcttt agttg tcatgcagct 240
 gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atcccaaat 300
 tgcagattta tcaacggctt ttatcttgaa aatagtgcc cgcagtctac aaattctggt 360
 atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca ttttgcctta 420
 gacaggccat ctgagacaca tgc agactat cttttgagaa ctgggcagggt tgtagatata 480
 tcagacacca tatacccgag gaaccctgcc atgtattgtg aagaagctag attaaagtcc 540
 tttcagaact ggccagacta tgctcaccta accccaagag agtttagcaag tgctggactc 600
 tactacacag gtattgggtga ccaagtgcag tgcttttgtt gtggtggaaa actgaaaaat 660
 tgggaacctt gtgatcgtgc ctggtcagaa cacaggcgac actttcctaa ttgcttcttt 720
 gttttgggcc ggaatcttaa tattcgaagt gaatctgatg ctgtgagttc tgataggaat 780
 ttcccaaatt caacaaatct tccaagaaat ccatccatgg cagattatga agcacggatc 840
 tttacttttg ggacatggat atactcagtt aacaaggagc agc ttgcaag agctggattt 900
 tatgcttttag gtgaagggtga taaagtaaag tgctttcact gtggaggagg gctaactgat 960
 tggaagccca gtgaagaccc ttgggaacaa catgctaaat ggtatccagg gtgcaaatat 1020
 ctgttagaac agaagggaca agaatatata aacaatattc atttaactca ttcacttgag 1080
 gagtgtctgg taagaactac tgagaaaaca ccatcactaa ctagaagaat tgatgatacc 1140
 atcttccaaa atcctatggt acaagaagct atacgaatgg gggttcagttt caaggacatt 1200
 aagaaaataa tggaggaaaa aattcagata tctgggagca actataaatc acttgagggt 1260
 ctggttgtag atctagtga tgctcagaaa gacagtatgc aagatgagtc aagtcagac t 1320
 tcattacaga aagagattag tactgaagag cagctaaggc gcctgcaaga ggagaagctt 1380
 tgcaaaatct gtatggatag aaatattgct atcgtttttg ttcccttgagg acatctagtc 1440
 acttgtaaac aatgtgctga agcagttgac aagtgtccca tgtgtacac agtcattact 1500
 ttcaagcaaa aaatttttat gtcttaatct aac tctatag taggcatggt atgttgttct 1560
 tattaccctg attgaatgtg tgatgtgaac tgactttaag taatcaggat tgaattccat 1620
 tagcatttgc taccaagtag gaaaaaaaat gtacatggca gtgttttagt tggcaatata 1680
 atctttgaat ttcttgattt ttcagggtat tagctgtatt atccattttt tttactgtta 1740
 tttaattgaa accatagact aagaataaga agcatcatac tataactgaa cacaatgtgt 1800
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 tcttttcaga taggcttaac aaatggagct ttctgtatat aaatgtggag attagagtta 1920
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 gaaagataga gattgttttt agaggttggt tgttgtgttt taggattctg tccattttct 2040
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 aaagcgtatt taatgataga atactatcga gccaacatgt actgacatgg aaagatgtca 2160
 gagatatgtt aagtgtaaaa t gcaagtggc ggacactat gtatagtctg agccagatca 2220
 aagtatgtat gttgttaata tgcatagaac gagagatttg gaaagatata caccaaaactg 2280
 ttaaatgtgg tttctcttcg gggagggggg gattggggga ggggccccag aggggtttta 2340
 gaggggcctt ttcacttttc acttttttca ttttgttctg ttcggttttt ttataagtat 2400
 gtagaccccg aagggtttta tgggaactaa catcagtaac ctaacccccg tgactatcct 2460
 gtgctcttcc tagggagctg tgttgtttcc caccaccac ccttccctct gaacaaatgc 2520
 ctgagtgtct gggcactttg 2540

181/292

<210> 275
<211> 842
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(842)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 275
tagaaagata ttttattttt taggaaaaga gccataatta tottaaa tgt gaaaaaccac 60
atccaataaa ctgatataaa gtttttaggaa caagggaata tcttattgtc acgcattcac 120
agtgaaccac attttaatgc aggtccagag ccaactgcag tcctgtccaa tcccataggt 180
acaagggcct ggctcctctt cctgtgtact gcccgacttc ctcatcttac tgggtccagc 240
ataaaagcaga tgtccactgt ctccct caca tgctgtgatc ttggcttaga ggtaggcaca 300
gtgccgctcc agcagcgagg ggctcgcgtt acttaggaac agcagctctt ttttcccttc 360
ttctgtagga gctntctcat gttgaagcca attgttttcc aaataatact gaatacaact 420
ttcaaattcc tttgggttat agttggaaac caggatggga ataaagggat ccaggggcatc 480
aaatccttcc tttcccagca actcctgcgg cagataggct ttccggggct taaagagaga 540
cccagtctgg ctccagagccg acacaatggc gcctccatgc caatcatnct tcatcatttt 600
cctcagttgt gaacaagtgc taattccctc ggggcaatcg ggctttatct tctgttttca 660
gagggttctt cccaangag cattgatgcc accacggcca cctatg ggtg aaacataccc 720
caatgaactt tgctctttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780
aaccgtgtta tgccctgtca aaccacttct ccagaagac tccctttctt aggccttttct 840
ct 842

<210> 276
<211> 1608
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1608)
<223> death associated protein 3 (DAP3) gene.

<400> 276
gaattccgcc ggccccaggc agcgtgtgtc ggtgcgctag gctggagaac tagtcct cga 60
ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga tccataagtt 120
ggaccctggg cgtttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180
agataaccag gttccagttg agagtcagag agctatttcc cgcaccaatg agaatgaccc 240
ggccaagcat ggggatcagc acgagggtca gcaacta caac atctcccccc aggattttgga 300
gactgtattt ccccatggcc ttctctctcg ctttgtgatg cagggtgaaga cattcagtga 360
agcttgcttg atggtgaaga aaccagccct agaacttctg cattacctga aaaacaccag 420
ttttgcttat ccagctatac gatattcttct gtatggagag aagggaacag gaaaaaccct 480
aagtctttgc catgttattc atttctgtgc aaaacaggac tggctgatac tacatattcc 540
agatgctcat ctttggttga aaaattgtcg ggatcttctg cagtccagct acaacaaaca 600
gcgctttgat caacctttag aggccttcaac ctggctgaag aatttcaaaa ctacaaatga 660
gcgcttcctg aaccagataa aagttcaaga gaagtatgtc tggaataaga gagaaa gcac 720
tgagaaaggg agtcctctgg gagaagtggg tgaacagggc ataacacggg tgaggaacgc 780
cacagatgca gttggaattg tgctgaaaga gctaaagagg caaagttctt tgggtatgtt 840
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agaagataaa agcccgattg ccccgagga atta gcactt gttcacaact tgaggaaaat 960
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ctttaagccc cggaagcct atctgcccc ggagttgctg ggaaaggaag gatttgatgc 1080
cctggatccc tttattccca tcctggtttc caactataac ccaaaggaat ttgaaagtgt 1140
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gaaaaaagag ctgctgttcc taagtaacgc gaaccctcgc ctgctggagc ggcaactgtgc 1260
ctacctctaa gccaaagatca cagcatgtga ggaagacagt ggacatctgc tttatgctgg 1320
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tgggattgga caggactgca gttggctctg gacctgcatt aaaatgggtt tcactgtgaa 1440
tgcgtgacaa taagatatcc ccttgctcct aaaactttat atcagtttat tggatgtggt 1500
ttttcacatt taagataatt atggctcttt tcctaaaaaa taaaatatct ttctaaaaaa 1560
aaaaaaaaa aaaaaaaaaa aaa aaaaaaa aaaaaaaaaa aaaaaaaa 1608
```

<210> 277

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 5' terminal sequence. gonadotropin -releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

<400> 277

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ttagattgca tgctattgta tgtctacagg gcatttgaca gccaaggnt aaatccaggt 60
gggacggtat ctaatgatgt cctgtccttc actgtccttg ccatcaccag ccacagagat 120
ccaggccttg gggactccca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
gctaggaagg catctggctc ggggactaac tactttgaac agtggtgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t 361
```

<210> 278

<211> 470

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> gonadotropin -releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

<400> 278

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gggatctttt tggctctctg cctctaaaca gaatgaagcc aattcaaaaa ctctagctg 60
gccttattct actgacttgg tgcgtggaag gctgctccag ccagcactgg tcctatggac 120
tgcgcccttg aggaagaga gatgccgaaa atttgattga ttctttcca a gagatagtca 180
aagaggtttg tcaactggca gaaacccaac gcttcgaatg caccacgcac cagccacgtt 240
ctcccctccg agacctgaaa ggagctcttg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa tttcagaaat 420
```

ccttacacca agttgcacat attccataat aaagtgcgtgt gttgtgaatg

470

<210> 279

<211> 320

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(320)

<223> 3' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 279

ntctaaatat caacagaaac tttattttctc atcgggttcag gaacaatcgg agggtagatg 60
gaaagaggaa gggagggaaa gagggagggg ggaagaatcc tgcgaaaagg aagggccaga 120
ctgaggggaga agaaaaacat gttcggggca aaagggtaat tctcaagtgg ggaatgccaa 180
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgaggtga 240
gtatgagacg caggtgggggt tgaatgaagg aaagtttagta ccncttaggg ctacaggacc 300
ctggggttct tctttcag ag 320

<210> 280

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 280

attcggcaca gggaaactttt cggcctggag tgggtgtgtct aagggactgg ctgagagtct 60
gcagccagac tacagtgaac gactctgcct cgtcagttag attcccccaa aaggaggggc 120
ccttggggag gggcctgggc tncctcatgc aaccagcata gccctactg ggccccccca 180
tgttacaccc taaagcctga aacctgaacc ccantactct gacagaagaa ccccagggtc 240
ctgtagccct aagtggtagt aactttcctt cattcaaccc acctgcgtct tatactcanc 300
tcancccaact gttggctgat tttggatttt tgtggcccca tgtaagggaac cctttaattt 360
ggcaatnccc aattgagaat taaccttttt gncccgaaca tgttttt 407

<210> 281

<211> 1451

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1451)
<223> interleukin 2 receptor, gamma (severe
combined immunodeficiency) (IL2RG) gene.

<400> 281
gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttcctgcagc 60
tgccctgtct gggagtgggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120
ccacagctga tttcttcctg accactatgc ccactgactc cc tcagtgtt tccactctgc 180
ccctcccaga gggtcagtggt tttgtgttca atgtcgagta catgaattgc acttgggaaca 240
gcagctctga gccccagcct accaacctca ctctgcatta ttggtacaag aactcggata 300
atgataaagt ccagaagtgc agccactatc tattctctga agaaatcaact tctggctgtc 360
agttgcaaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac 420
gggaaccag gagacaggcc acacagatgc taaaactgca gaatctgggtg atcccctggg 480
ctccagagaa cctaacactt cacaactga gtgaatccca gctagaactg aactggaaca 540
acagattctt gaaccactgt ttggagcact tgggtcagta cgggactgac tgggaccaca 60 0
gctggactga acaatcagtg gattatagac ataagttctc cttgcctagt gtggatgggc 660
agaaacgcta cagttttcgt gttcggagcc gctttaaccc actctgtgga agtgctcagc 720
attggagtga atggagccac ccaatccact gggggagcaa tacttcaaaa gagaatcctt 780
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gactggctga gactctgcag ccagactaca gtgaacgact ctgcctcgtc agtgagattc 1020
ccccaaaagg agggggccc tt ggggaggggc ctggggcctc cccatgcaac cagcatagcc 1080
cctactgggc ccccccatgt tacaccctaa agcctgaaac ctgaacccca atcctctgac 1140
agaagaaccc cagggtcctg tagccctaag tgggtactaac tttccttcat tcaaccacc 1200
tgctctcat actcacctca cccactgtg gctgatttgg aattttgtgc ccccatg taa 1260
gcaccccttc atttggcatt cccacttga gaattaccct tttgccccga acatgttttt 1320
cttctccctc agtctggccc ttcccttttcg caggattctt cctccctccc tctttccctc 1380
ccttctctt tccatctacc ctccgattgt tcctgaaccg atgagaaata aagtttctgt 1440
tgataatcat c 1451

<210> 282
<211> 317
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(317)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 282
atctaacaca acacttttaga aagatatttt atttttttagg aaaagagcca taattatctt 60
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120
attgtcacgc attcacagt aaaccattt taatgcaggc ccagagccaa ctgcagtcct 180
gtccaatccc atagggtaca agggcctggg ctctcttccc tgtgtactgc ccgacttccc 240
catcttactg ggggtccagca taaagcagga tgtccactgt cttcctcaca tgctgtganc 300
ttggncttag gaggtag 317

<210> 283
<211> 358
<212> DNA
<213> Artificial Sequence

185/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(358)

<223> 5' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 283

```
aggacgggacg ctttggagcc ggccccaggc agcgtgtgtc ggtcgccctag tctggagaac 60
tagtcctcga ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga 120
tccataagtt ggaccctggg cgtttttttac acatggggac ccaggctcgn caaagcattg 180
ctgctcacct agataaccca ggttcccagt tgagagtccc gagagctatt ttcccgcac 240
caatgagaat gaccccgggc caagcatggg ggatcancaa ggaggggtcaa gcaa tnacaa 300
cantttttccc cccaggattt tgggagaatt gtaattttcc ccatnggcct ttncttcc 358
```

<210> 284

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 5' terminal sequence. ptk2 protein tyrosine
kinase 2 (PTK2) gene.

<400> 284

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gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60
cagtatgtca tgaccagcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120
gccttggtctg tggatgccaa aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg 240
aagatgttct ctagccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300
gcacttacag ctccaacttt tttgaatgac catctgggtg aaaaatcttt ctcatataag 360
tttnaaccac atttggattt ggggttcatt ttttgttttg tttttttttc aatcat 416
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<210> 285

<211> 3052

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3052)

<223> ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 285

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ccggtgtgaa ggccatgagt gattactggg ttgttggaaa gaagtctaac tatgaagtat 60
tagaaaaaga tgtttggttta aagcgatttt ttcctaagag ttactggat tctgtcaagg 120
ccaaaacact aagaaaactg atccaacaaa catttagaca atttgccaac cttaatagag 180
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaat 240
gcttcaagtg tgctcttggt tcaagctgga ttatttcagt ggaactggca atcggccag 300
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186/292

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aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgaacttca 360
ctcaagtgc aaccattcag tattcaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcaggtgca cccgagcctc tgacagtgc ggcaccatcc ctaaccattg 480
cggagaatat ggctgacctc atagatgggt actgccggt ggtgaatgga acctcgcatg 540
catttatcat cagacctcag aaagaagggt aacgggcttt gccatcaata ccaaagttgg 600
ccaacagcga aaagcaaggc atgcggacac acgccgtctc tgtgtcag aa acagatgatt 660
atgctgagat tatagatgaa gaagatactt acaccatgcc ctcaaccagg gattatgaga 720
ttcaaaagaa aagaatagaa cttggacgat gtattggaga aggccaattt ggagatgtac 780
atcaaggcat ttatatgagt ccagagaatc cagctttggc ggttgcaatt aaaacatgta 840
aaaactgtac ttccggacagc gtgaga gaga aatttcttca agaagcctgc cattacacat 900
ctttgcactg gaattgggtgc agatatataa gtgatcctaa tgttgatgcc tgcccagacc 960
ccaggaatgc agagttaaca atgcgtcagt ttgaccatcc tcatattgtg aagctgattg 1020
gagtcatcac agagaatcct gtctggataa tcatggagct gtgcacactt ggagagctga 1080
ggtcattttt gcaagtaagg aaatacagtt tggatctagc atctttgatc ctgtatgcct 1140
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ctgctcggaa tgttctggtg tcctcaaagt attgtgtaaa attaggagac tttggattat 1260
cccgatataa ggaagatagt acttactaca aagcttccaa a ggaaaattg cctattaaat 1320
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ctcctaccct ctacag cctt atgacgaaat gctgggccta tgaccccagc aggcggccca 1560
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gattttatcc cagcccacag cacatggtag aaaccaatca ttaccagggt tctggctacc 1800
ctggttcaca tggaaatcaca gccatggctg gcagcatcta tccaggtcag gcatctcttt 1860
tggaccaaac agattcatgg aatcatagat ctcaggagat agcaatgtgg cagcccaatg 1920
tggaggactc tacagtattg gacctgcgag ggattgggca agtgttgcca acccatctga 1980
tggaaagagc tctaattcga cagcaacagg aaatggaaga agatcagcgc tggctggaaa 2040
aagaggaaag atttctgatt ggaaaccaac atatatatca gcctgtgggt aaaccagatc 2100
ctgcagctcc accaaagaaa ccgcctcgcc ctggagctcc cggtcacttg ggaagccttg 2160
ccagcctcag cagccctgct gacagctaca acgaggggtg caagcttcag cccaggaaa 2220
tcagccccc tcctactgcc aacctggacc ggtcgaatga taagggtgac gagaatgtga 2280
cgggcctggt gaaagctgtc atcgagatgt ccagtaaaat ccagccagcc ccaccagagg 2340
agtatgtccc tatggtgaag gaagtcggct tggccctgag gac attattg gccactgtgg 2400
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tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag cagtatgtca 2520
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tggatgcaa aaacttac tc gatgtcattg accaagcaag actgaaaatg cttgggcaga 2640
cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg aagatgttct 2700
ctagccttcc accagcagcg aggaattaac cctgtgtcct cagtgcagc cactcacagc 2760
tccaactttt ttgaatgacc atctgggtga aaaatctttc tcatataagt ttaacca cac 2820
tttgatttgg gttcattttt tgttttgttt ttttcaatca tgatattcag aaaaatccag 2880
gatccaaaat gtggcgtttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatacg ttctaaaggg ggatggccaa ggggtgacat 3000
cttaattcct aaactacctt agctgcatag t ggaagagga gagccggaat tc 3052

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<210> 286

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 286

```

gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagagggaa catacccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctccata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttcntcc 240
atgggcagcc actccattgc tcaactccgn ttaccttcat cttatgtag gataagagtn 300
ctgcagagct tcgaaagggc agagattcgc ttgtgtgggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377

```

<210> 287

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 287

```

catatctgga caaggcacc ccaccaggt tgcagccgaa acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcgttcacc gagatctgaa 120
gccagagaac attctggtga caagtggtn gacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccgtggtt gttacactct ggtacc gagg 240
tcccgaagtt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttgg 300
ctgtatcttt gcagagatgt ttctgtcgaa nccctctctt ctgtggnaaa ctctgtaagg 360
ccg 363

```

<210> 288

<211> 1443

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1443)

<223> cyclin-dependent kinase 4 (CDK4) gene.

<400> 288

```

gccctcccag ttccgcgcg cctctttggc agctggtcac atggtgaggg tgggggtgag 60
ggggcctctc tagcttgcg cctgtgtcta tggtcgggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgatgg ggccgtagga accggctccg gggcccgat aacgggccgc 180
ccccacagca cccgggctg gcgtgagggc ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca gtggctgaaa ttgggtgtcg tgcctatggg acagtgt aca aggcccgtga 300
tccccacagt ggccactttg tggccctcaa gactgtgaga gtccccaatg gaggaggagg 360
tgaggagggc cttcccatca gcacagttcg tgagggtggc ttactgaggc gactggaggc 420
ttttgagcat cccaatggtt tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tgttt gagca thtagaccag gacctaaagg catatctgga 540
caaggcacc ccaccaggt tgccagccga aacgatcaag gatctgatgc gccagtttct 600
aagaggccta gatttccttc atgccaatg catcggtcac cgagatctga agccagagaa 660
cattctggtg acaagtgggt gaacagtcac gctggctgac ttggccctgg ccagaatcta 720

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188/292

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cagctaccag atggcactta caccogtggg tgttacactc tggtaaccgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggtggct gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttctg tggaaactct gaagccgacc agttgggcaa 900
aatctttgac ctgattgggc tgcctccaga ggatgactgg cctcg agatg tatccctgcc 960
ccgtggagcc tttcccccca gagggccccg cccagtgcag tcggtggtac ctgagatgga 1020
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tgcctttcga gctctgcagc actcttatct acataaggat gaaggtaatc cggagtgcgc 1140
aatggagtgg ctgccatgga aggaagaaaa gctgccattt ccttctgga cactgagagg 1200
gcaatctttg cctttatctc tgaggctatg gaggtcctc ctocatctt ctacagagat 1260
tactttgctg ccttaatgac attccccctc cacctctcct tttgaggctt ctccttctcc 1320
ttcccatctt tctacactaa ggggtatgtt cctcttctc cctttcccta cctttatatt 1380
tggggtcctt ttttatacag gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443

```

<210> 289

<211> 394

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(394)

<223> 3' terminal sequence. basic transcription factor 3 (BTF3) gene.

<400> 289

```

cccgcgtgtg tgcgcctaan ctcaggnggn ccaccogaga ccccttgagc accaacccta 60
gtccccgcgc cggcccctna ttgcgtccga caagatgaaa gaaaca atca tgaaccaggg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctgcgagaaa 180
gaagaagggt gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaaa 240
gangttaggg gtaaacaata tctctggnat tgaagagggt aatatgttta caaaccaggg 300
aacagtgatc cactttaaca acc tnaagt tcagggcac tctgggcagc ggacactttc 360
accattacng gccttgctga gncaaagcag ctgg 394

```

<210> 290

<211> 477

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(477)

<223> basic transcription factor 3 (BTF3) gene.

<400> 290

```

atgcgacgga caggcgcacc cgctcagggt gactctcggg ggcgagggtc agccaggggc 60
ggctgccctg ggggcgaggc gacgtgtct caacctcac ctgcggcgag aaccgagga 120
gaggagcctc agatgaaaga aacaatcatg aaccag gaaa aactcgccaa actgcaggca 180
caagtgcgca ttggtgggaa agtgaatatg tttacaaacc aaggaacagt gatccacttt 240
aacaacccta aagttcaggc atctctggca gogaacactt tcaccattac aggccatgct 300
gagacaaagc agctgacaga aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgcccacaa aatctgtgga tggaaaagca 420
ccacttgcta ctggagagga tgatgatgat gaagttccag gaggcttcca agaataga 477

```

<210> 291
<211> 388
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(388)
<223> 3' terminal sequence. colony stimulating
factor 1 receptor, formerly mcdonough feline
sarcoma viral (v-fms) oncogene homolog (CSF1R)
gene.

<400> 291
tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60
agcttggggg agtttgtgct tcctgcttgg nggtggccagc cacatgccaa ggtcccctgc 120
cttctagccc agaatgacgg gactgggcag aacaccccca acttttagct gccacttggc 180
tcattacagc agtaccagta tgggggtggg aggggtgagg ctntggagtg aaggcggcgt 240
atagggcaga gactaagagg gtcctgtg ag attccttagag gagccatcct gntccaaggg 300
gcctgagctg agtntgggtc tgtgagcatc tgctgctcct ctgagagagg ggagatctca 360
ctctctgccg gtctgtctag ccccaaag 388

<210> 292
<211> 3992
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3992)
<223> colony stimulating factor 1 receptor,
formerly mcdonough feline sarcoma viral (v -fms)
oncogene homolog (CSF1R) gene.

<400> 292
ggcttcagga agggcagaca gagtgtccaa aagcgtgaga gcacgaagtg aggagaaggt 60
ggagaagaga gaagaggaag aggaagagga agagaggaag cggaggggaac tgcggccagg 120
ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180
cagtgcagag gagaggaacg tgtgtccagt gtcccgatcc ctgcgagagct agtagctgag 24 0
agctctgtgc cctgggcacc ttgcagccct gcacctgcct gccacttccc caccgaggcc 300
atgggcccag gaggttctgct gtcctgtctg gtggccacag cttggcatgg tcagggaatc 360
ccagtgatag agcccagtggt ccccgagctg gtcgtgaagc caggagcaac ggtgaccttg 420
cgatgtgtgg gcaatggcag cgtggaatgg gatggccccg catcacctca ctggacctg 480
tactctgatg gctccagcag catcctcagc accaacaacg ctaccttcca aaacacgggg 540
acctatcgct gcactgagcc tggagacccc ctgggaggca gcgcgcgcat ccacctctat 600
gtcaaagacc ctgcccggcc ctggaacgtg ctagcacagg aggtggtcgt gttcgaggac 660
caggacgcac tactgccctg tctgtctaca gaccgggtgc tgggaagcagg cgtctcgctg 720
gtgcgtgtgc gtggccggcc cctcatgcgc cacaccaact actccttctc gccctggcat 780
ggcttcacca tccacagggc caagttcatt cagagccagg actatcaatg cagtgccttg 840
atgggtggca ggaaggtgat gtccatcagc atccggctga aagtgcagaa agtcatccca 900
gggccccag ccttgacact ggtgcctgca gagctggtgc ggattcgagg ggaggctgcc 960
cagatcgtgt gctcagccag cagcgttgat gtttaactttg atgtcttctt ccaacacaac 1020

190/292

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aacactaagc tcgcaatccc tcaacaatct gactttcata ataaccgtta ccaaaaagtc 1080
ctgaccctca acctcgatca agtagatttc caacatg ccg gcaactactc ctgcggtggcc 1140
agcaacgtgc agggcaagca ctccacctcc atgtttcttc ggggtggtaga gagtgcctac 1200
ttgaacttga gctctgagca gaacctcacc caggaggtga ccgtggggga ggggctcaac 1260
ctcaaagtca tgggtggaggc ctaccagggc ctgcaagggt ttaactggac ctacctggga 1320
ccctttttctg accaccagcc tgagcccaag cttgctaatt ctaccacca ggacacatac 1380
aggcacacct tcacctctc tctgccccgc ctgaagccct ctgaggettg ccgctactcc 1440
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ccccagagg taagcgatcat atggacattc atcaacggct ctggcaccct tttgtgtgt 1560
gcctctgggt acccccagcc caacgtgaca tggctgcagt gcagtggcca cactgatagg 1620
tgtgatgagg cccaagtgtc gcaggtctgg gatgacccat accctgaggt cctgagccag 1680
gagcccttcc acaaggtgac ggtgcagagc ctgctgactg ttgagacctt agagcacaac 1740
caaacctacg agtgcagggc ccaca acagc gtggggagtg gctcctgggc cttcataccc 1800
atctotgcag gagccacac gcacccccg gatgagttcc tcttcacacc agtgggtggc 1860
gcctgcatgt ccatcatggc cttgctgctg ctgctgctcc tgctgctatt gtacaagtat 1920
aagcagaagc ccaagtacca ggtccgctgg aagatcatcg agagctatga gggcaacagt 1980
tatactttca tcgacccccc gcagctgcct tacaacgaga agtgggagtt ccccggaac 2040
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caagtagccc agggcatggc cttcctcgtc tccaagaatt gcacccaccg gg acgtggca 2640
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ccagtcccg cttctgggc tagaaggcag gggaccttgg cattggctgg ccacaccaag 3900
caggaagcac aaactcccc aagctgact c atcctaacta acagtcacgc cgtgggatgt 3960
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<210> 293

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

191/292

<221> misc_feature
 <222> (1)..(356)
 <223> 3' terminal sequence. friend leukemia virus
 integration 1 (FLI1) gene.

<400> 293
 tttatttagt caaattatatt tacaacatgg ncttctttga cagttgtcag cttaacactt 60
 aatatagtta aaaaagtcaa caattacctg caaaattata tatatntnaa tgtctaaaaa 120
 tatgtngctt atatagagca ggaaaatccc tcctctccac aagggaagt ttcgttgttt 180
 tnccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagacta 240
 aatgggatta tctttncctt gcttgtgtat gcctgtnaaa taactgtacc agtggctttg 300
 ctttctcata ggtcagtgac ttaaacagcc ctgtttcctt ttcggctata g ggcac 356

<210> 294
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(465)
 <223> 5' terminal sequence. friend leukemia virus
 integration 1 (FLI1) gene.

<400> 294
 gaccaaagca gtttcttgtc aatacacggg gttcagtatg acacagaatc atggacttaa 60
 cccgtcatgt tctggtttga gatttagtga caaatagagg tgggaagctt ataactaat 120
 tttaggagga ccaaattcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180
 tttcacccaa ctggaatttg atggaaagaa gggt tgtgtg ttttaagacgc caagggcatt 240
 gcagaatccc tctcagtggc cagtatgcac tcagctgacc actctctcta gccaatagtc 300
 aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360
 attaaattna ctaattttnt tttttttttt ttaaattgatn gacagtggnt ccccggaact 420
 tgggaaangt tgtaggggnt ttctaaaccc aagncgattc gcant 465

<210> 295
 <211> 2957
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2957)
 <223> friend leukemia virus integrati on 1 (FLI1)
 gene.

<400> 295
 gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcaggag 60
 ggcccagggc gccaggagg ccgcgcggg ctaatccgaa ggggctgcga ggtcaggctg 120
 taaccgggtc aatgtgtgga atattgggg gctcggctgc agacttggcc aaatggacgg 180
 gactattaag gaggctctgt cgggtggtgag cgacgaccag tccctctttg actcagcgta 240
 cggagcggca gccatctcc ccaaggccga catgactgcc tcggggagtc ctgactacgg 300
 gcagccccac aagatcaacc cctcccacc acagcaggag tggatcaatc agccagtgg 360
 ggtcaacgct aagcgggagt atgaccacat gaatggatcc agggagtctc c ggtggactg 420

192/292

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cagcgtttagc aaatgcagca agctgggtggg cggaggcgag tccaacccca tgaactacaa 480
cagctatatg gacgagaaga atggccccc tcttcccaac atgaccacca acgagaggag 540
agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatggctgga 600
gtggggcata aaggagtaca gcttgatgga gatcgacaca tcttttttcc agaacatgga 660
tggcaaggaa ctgtgtaaaa tgaacaagga ggacttcctc cgcgccacca ccctctacaa 720
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cggcattgcc caggctctgc agc cacatcc gaccgagtcg tccatgtaca agtacccttc 1320
tgacatctcc tacatgcctt cctaccatgc ccaccagcag aagggtgaact ttgtccctcc 1380
ccatccatcc tccatgcctg tcaattcctc cagcttcttt ggagcgcgt cacaatactg 1440
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cgtgccttca cacttaggca gctactacta gaagcttctt ctagctgaag cccatcctgc 1560
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tggatgttct ttcttgttgg atagaacctt tgtatttgtt ctttaaaaaac atttttttta 1680
atgttggtaa cttttgcttc ctctacctga acaaaga gat gaataattcc atggggccagt 1740
atgccagttt gaattctcag tctcctagca tcttgtgagt tgcataataa gattactgga 1800
atggttaagt catggttctg agaaagaagc tgaactgttt ctttatgttt ttatgaccaa 1860
agcagtttct tgtcaatata cggggttcag tatgacacag aatcatggac ttaacccgtc 1920
atgttctggg ttgagattta gtgacaaata gaggtgggaa gcttataatc taattttagg 1980
aggacaaat tcagcggatg gcaactggaa cattgattgt aaggccagt aagttttcac 2040
ccaactggaa tttgatggaa agaaggtttg tgtgtttaag acgccaaggg cattgcagaa 2100
tccctctcag tggacagtat gcactcagct gaccactctc tctagaaata gtcaagatat 2160
gaactaagaa attttaaatgc aaatacatat attcctgaaa gacggggaat taaattacta 2220
attttttttt ttttaaatgat gacagtgggc ccagaacttg gaaaagttgt agggatttct 2280
aaactcaagc agattcgcaa gtgctgtgag cttgtcagac catcagacca gggccaacca 2340
atcagaaggc aacttactgt ataaa ttatg cagagttatt ttcctatata tcacagtatt 2400
aaaaataaaa taattaaaaa ttaagaataa ataaacgagt tgacctcggc cacaaaagca 2460
gttttactat cgaatcaatc gctgttattt ttttttaatg taatttgtac atcttttttc 2520
aatctgtaca tttgggctgt cttgtatgtt ttttatgtct tttttaaaaa gcataatatg 2580
cctatagctg aaaaggaaac agggctgttt aagtcactga cttatgagaa agcaaagcac 2640
tggtacagtt atttaacagg catacacaag cagggaaaag ataatccatt tagatcttta 2700
atgctttgga aatgcgtgta acagtactgc aataatcaca gctctgggaa aaacaacgaa 2760
actttccctt gtggagagga gggattttcc tgctctata t aagcaacata ttttagaca 2820
ttaaaatata tataattttg caggtaatgt ttgaactttt taactatatt aagtgttaag 2880
ctgacaactg tcaaagaaga ccatgttgta aaataatttg actaaataaa tggttccttc 2940
tctcaaaaaa aaaaaaa 2957

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<210> 296

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 3' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 296

193/292

```

cacccttct cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc ccctttgttc agtgtggctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgcctgagcg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtaggaatc tctaacagct ggcatacatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttggtttt tgttttttta gatacaaatc ccactaatga 300
aaaaaattta aaaatcaatt tactcattta ggctgtgagg tcatcaggct aaagcaccat 360
ctctctcttg ggctttatcc ctggggcagg ggaggggggg                400

```

<210> 297

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(464)

<223> 5' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 297

```

cgtggtagat tttcatagtg ccgaatatat gcttaagcaa ataaggcaac acagtttagca 60
tggtctgcgat gtttagccaat gtccattgcc agaaactgag ttctctatca gcaagagatg 120
tgctcatctt gttctggact atatctctc a gggactaga gggcagcctg ctaaattggta 180
tgactcaaat aaatatTTTT ggaatgaatt aaagagtggc atggcttaca gaagtataga 240
tgtagtata gtcattccgtt gagcctttgc ttttttttct gggaacactg aaggaagact 300
cacagccacc catgggtgtt tgaccctcca cttgccttgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgttg aacagacaag gccacntct atggcttcgg nacaggtagn 420
aaaactgtcc tgtgtggccc cgctnggcag ggatcaccag tttag                464

```

<210> 298

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 298

```

aaatacctaaa actacaaaaa tcagtttata aactgttttt ccaaaaacaac caccaaaaaca 60
aaacaatccc ccaaatcagg gcaaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaaataaaa agtcatccac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttggcgac cacatggccg ggtggttccc aagagtagcc atgggttatg attttgagaa 240
ccacggaggg ggnaaacagc tgttctgact gcccccttt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttccaat g ttttaagatgt atttttaanc cttaattggtt 360
tnaggcctcc ccaacttt                378

```

<210> 299

<211> 317

194/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(317)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 299

```
actggaagag gttgctcggc gctggggcat ccagaagaac cggccagcca tgaactatga 60
caagctgagc cgctctctcc gctattacta tgaaaagggc atcatgcaga aggtggctgg 120
agagcgatac gtctacaaat ttgtctgtga ccagatgcc ctcttctcca tggctttccc 180
ggataaccag cgtccgttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
cctgccgctg acccactttg aagacagccc cgcttacctc ctggacatgg accgctgcag 300
cagcctcccc tatgccg                                     317
```

<210> 300

<211> 4071

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4071)

<223> ets variant gene 5 (ets -related molecule)
(ETV5) gene.

<400> 300

```
gagtccagcc gctggtgccc ggagcgggtc accgtcttcg gagcggttcg gccagcctt 60
tcgcccaggc gccaggccc gctgcgcgcg tcgctgagcg cgcctgcgcc gccagggccc 120
ctgcaagggg aggagagcgg ccgcctcagg aggatccctt tccccccaga aattactcaa 180
tgtgaaacc tctcaaagtg gtattagaga cgctgaaagc accatggacg ggttttatga 240
tcagcaagtc ccttttatgg tcccaggga atctcgatct gaggaatgca gagggcggcc 300
tgtgattgac agaaagagga agtttttggg cacagatctg gctcacgatt ctgaagagct 360
atctcaggat ctcagtcac ttcaagaggc ttgggttagct gaagcacaag ttctgatga 420
tgaacagttt gtcccaga tt ttcagtcgta taacctgggtg cttcatgccc cacttccaac 480
caagatcaaa cgggagctgc acagcccctc ctctgagctg tcgtcttgta gccatgagca 540
ggctcttggt gctaactatg gagaaaagtg cctctacaac tattgtgcct atgataggaa 600
gcctccctct gggttcaagc cattaacccc tcctacaacc cccctctcac ccacccatca 660
gaatccccta tttccccac ctcaggcaac tctgccacc tcagggcatt cccctgcagc 720
tggcccagtt caaggtgtgg gccccgccc cgcctcccat tcgcttcag agcctggacc 780
acagcagcaa acatttgcgg tccccgacc accacatcag cccctgcaga tgccaaagat 840
gatgcctgaa aaccagtatc catcagaaca gagatttc ag agacaactgt ctgaaccctg 900
ccaccccttc cctcctcagc caggagttcc tggagataat cgccccagtt accatcgcca 960
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ccagtcacca atgggaatca agcaggagcc tcgggattac tgcgtcgatt cagaagtgcc 1140
taactgccag tcctcctaca tgagaggggg ttatttctcc agcagccatg aaggtttttc 1200
atatgaaaaa gatccccgat tatactttga cgacacttgt gttgtgcctg agagactgga 1260
aggcaaagtc aaacaggagc ctaccatgta tcgagagggg ccccttacc aga ggcgagg 1320
ttcccttcag cctgtgcag tcctggctac ccttcttgat gaccagcca atgccactt 1380
cattgcctgg acaggtcgag gcatggagtt caagctgata gaaccggaag aggttgctcg 1440
gcgctggggc atccagaaga accggccagc catgaactat gacaagctga gccgctctct 1500
```

195/292

```

ccgctattac tatgaaaagg gcatcatg ca gaaggtggct ggagagcgat acgtctacaa 1560
atgtgtctgt gaccagatg ccctcttctc catggctttc cgggataacc agcgctccgtt 1620
cctgaaggca gagtccgagt gccacctcag cgaggaggac accctgccgc tgaccactt 1680
tgaagacagc cccgcttacc tcctggacat ggaccgctgc agcagcctcc cctatgccga 1740
aggctttgct tactaagttt ctgagtggcg gagtggccaa accctagagc tagcagttcc 1800
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cattggctgg ggagtgggaa cagggagggg cagaaaacca c caaaaggcc agtgcctcaa 1980
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aagccccctt tctcttccca atcacgtggc tgagtgtgga tgacttttat tttaggagaa 2460
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ttgcattccc attggactca tgcacctccc ggatggtttt tgtttttttt ggggggttctt 3900
tggggtttgt ttgtttgctt cttttccaga gtgtggaaaag tctacagtgc agaaaggctt 3960
gaacctgcca gctgatttga aatactttca ccctgcgcag ggccgtatgc atcctgcaa 4020
gctgcgttat attctgtact gtgtacaata aagaagtttg cttttcgttt a 4071

```

<210> 301

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 3' terminal sequence. cyclin-dependent
kinase 4 (CDK4) gene.

<400> 301

nccngtataa aaaaggaccc caaatataaa ggtagggaaa gggacaagag ggaacata cc 60

196/292

```
ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
atgtcattaa ggcagcaaag taatctctgt agaaagatgg aggaggaccc tccatagcct 180
cagagntaaa ggcaaagnnt gccctctcag tntcngaag ggaaatggca gcttttcttc 240
cttccatggg cagccactcc attgctcact ccggatt acc ttcatactta tgtaggataa 300
gggtgctgca gagctcgaaa gggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
nccgcgagca gctttgcttc cccgactcct nccttttcag gnacccc 407
```

<210> 302

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(405)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 302

```
attcgncaca gaggaggagg tggaggagggc ottcccatca gcacagttag tgaggtggct 60
ttactgagggc gactggagggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca tgtagaccag 180
gacctaagga catatctgga caaggcacc caccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaatg catcgttcac 300
cgaggatctg aagccagaga acattctggg tgacaagtgg ttggancagt caagctggct 360
ggactttggg cctgggcagn aatctancag cttaccagat gggca 405
```

<210> 303

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi
sarcoma viral oncogene homolog 1 (YES1) gene.

<400> 303

```
caatgagaac tttttatttc aattatccac aaaacaatat tacaatactt tataaaaata 60
ttaagttagt gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttccaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatattaca agttgtttt tcttgggcaa tttaaaaata caggancaat 240
ttaaantgaa tacacattaa gtttaggtgt tttatcccta ctatacaatt gttattatat 300
agggaaactgc tcccttcn gg ttaaanccct aatggaatac ccatcaactt ttcccgcccc 360
ntactttccc nggattgggg tttagggtac ctaaacggga aatttaggtc nccccntttg 420
```

<210> 304

<211> 4517

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene
homolog 1 (YES1) gene.

<400> 304

```

gcggagccaa ggcacacggg tctgaccctt gggccggccc ggagcaagtg acacggaccg 60
gtcgccctatc ctgaccacag caaagcggcc cggagcccgc ggaggggacc tgacgggggc 120
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cggacggcgg cgcgcgcgaga tttgataatg ggctgcatta aaagtaaaga aaacaaaagt 240
ccagccatta aatacagacc tgaaaatact ccagagcctg tcagtacaag tgtgagccat 300
tatggagcag aacccactac agtgtcacca tgtccgtcat ctt cagcaaa gggaacagca 360
gttaattttca gcagtctttc catgacacca tttggaggat cctcaggggt aacgcctttt 420
ggaggtgcat cttcctcatt ttcagtgggtg ccaagttcat atcctgctgg ttttaacaggt 480
ggtgttacta tttttgtggc cttatatgat tatgaagcta gaactacaga agacctttca 540
tttaagaagg gtgaaagatt t caaataatt aacaatacgg aaggagattg gtgggaagca 600
agatcaatcg ctacaggaaa gaatggttat atcccagagca attatgtagc gcctgcagat 660
tccattcagg cagaagaatg gtatttttggc aaaatgggga gaaaagatgc tgaaagatta 720
cttttgaatc ctggaaatca acgaggatatt ttcttagtaa gagagagtga aacaactaaa 780
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tgatgggaa catggaatgg aaccacgaaa gtagcaatca aaacactaaa accaggtaca 1140
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gctacagagc cacagtacca gccaggagaa aatttataat tcaagtagcc tattttatat 1860
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ctttgctggc actcagagct cctcaacttag ctatatcttg agactttgaa gagttataaa 3000
gtataactat aaaactaatt tttcttacac actaaatggg tatttgttca aaataatgaa 3060

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198/292

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gttatggcctt cacattcatt gcagtgggat atgggttttta tgtaaaacat ttttagaact 3120
ccagtttttca aatcatgttt gaatctacat tcacttttttt ttgtt ttott ttttgagacy 3180
gagtctcgct ctgccgcca ggctggagt cagtggcgcg atctcggtc actgcaagct 3240
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tgcccaccac cagcctggc tagttttttg tttttttagt agagacgcag tttcaccgtg 3360
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ctaaatctaa tcaggaaagt aaggcaggaa aagttgatgg tattcattag gttttaactg 4200
aatggagcag ttccttatat aataacaatt gtatagtagg gataaaa cac taacaatgtg 4260
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aaaaaggaag ttggcaaaaa cagccttcta gcacactttt ttaaatgaat aatggtagcc 4440
taaaacttaat atttttataa a gtattgtaa tattgttttg tggataattg aaataaaaag 4500
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```

<210> 305

<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(459)

<223> 3' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 305

```

ncttgtctga aggtgtgctg gacacctcct ggggctcttc tgggtcattt ggttctggag 60
aattatctct tatctctggc atagagccca agggagagtg gggcatctct tgagggctct 120
ctttatctct tatttggggg atcaggttgt cactggccac ttgcacagtg ctagtgagga 180
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tactgaagt gcttcttctc tcctgggatg agtgcaggga gaggcaggac agggtcagat 300
gggctggcg actcactcag gatctcatcg ctttgcctgg agg atgttcc agggctcact 360
gactcttggg cgcacaagg gaaacagctt ggtttgaagg gggttnttgg tngggggcaa 420
gcnaatngg gtatggaagg aagcttcct ctaanaagg 459

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<210> 306

<211> 370

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

199/292

<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 306
tgcgtttgtc aaagcacaga cttcctgttt tgccctgctag catctccctg taactctccc 60
aatcttgagg agtgatccct gtccc agccc ctggaaaggg anggaaacga caaactcaaa 120
gtccaggatg ttccaccatga caagagccat ggaagaggct ctttttcagc acttcatgca 180
ccagaagctg gggatcgcct atgccatata caagccattt cccttctttg aaggcctcct 240
agacaactcc atcatcacta agagaatgta catggaatct ctggaagcct gtagaaattt 300
gatccctgta tccagagtgg tgcacaacat tctcacccaa ctgggagagg actttttaac 360
ctgtctcttt 370

<210> 307
<211> 1541
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1541)
<223> interferon-induced protein 75, 52kd (IFI75)
gene.

<400> 307
aattccggca tgcgtttgct gggaggatgt tccaggctca ctgactcttg gcgcacaggg 60
tgaacagctt ggttgagtcg cccagcccat ctgaccctgt cctgcctctc cctgcactca 120
tccaggaagg aagaagcact tcagtgacca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tcaactagcac tgtgcaagtg gccagtgaca 240
acctgatccc ccaaataaga gataaagaag accctcaaga gatgccccac tctcccttgg 300
gctctatgcc agagataaga gataattctc cagaacccaa t gacccagaa gagccccagg 360
aggtgtccag cacaccttca gacaagaaag gaaagaaaag aaaaagatgt atctgggtcaa 420
ctccaaaaag gagacataag aaaaaagcc tcccaagagg gacagcctca tctagacacg 480
gaatccaaaa gaagctcaaa aggggtggatc aggttctctc aaagaaagat gactcaactt 540
gtaactccac ggtagagaca agggcccaaa aggcgagaac tgaatgtgcc cgaaagtcga 600
gatcagagga gatcattgat ggcacttcag aaatgaatga aggaaagagg tcccagaaga 660
cgccctagtac accacgaagg gtcacacaag gggcagcctc acctgggcat ggcatccaag 720
agaagctcca agtgggtggat aagggtgactc aaaggaaaga cgactcaacc tggaactcag 780
aggtcatgat gaggggtccaa aaggcaagaa ctaaatgtgc ccgaaagtcc agatcgaaag 840
aaaagaaaaa ggagaaagat atctgttcaa gctcaaaaag gagatttcag aaaaatatc 900
accgaagagg aaaacccaaa agtgacactg tggattttca ctgttctaag ctccccgtga 960
cctgtggtga ggcgaaaggg attttatata agaagaaaaat gaaacacgga tcttcagtga 1020
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aaggaaggaa cgcaaaagac tggaaacgga atatacgttg tgaaggaatg accctaggag 1140
agctgctgaa gcggaaaaac tcggatgaat gcgagggtgtg ctgtcaaggg ggacaacttc 1200
tctgctgcgg tacttgtcca cgagtcttcc atgaggactg tcacatcccc cctgtggaag 1260
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atttaatatc cgagattacg gtgagccttt caggaagcaa tgtggttgga cctgggttaag 1500
ggaaaggctg attacgaaa tgtacacggt ggcccggaaat t 1541

<210> 308
<211> 416
<212> DNA

200/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 3' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 308

```
gttannncnan tnnattttttt aagagagagg caatttttatt cttccaaaaa aatgcaccag 60
agaggggtgag cacaggagca cccctggcca catcccccat cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tccctgtggc cttggggagg 180
gaaccaggca gacctgggaa gtggaacttt gttgttagca ccaggagccg cccacagctg 240
ggcttcggca acagggcagc acatggccct gttccttcca cctgagagt c tggggagggg 300
ctgggtggcag aaggctccct gcaggagggtt cacctgaatg actctcagat tcacagaccc 360
cctnttgccc ccacaacccc tgtaaacatg agaatggggc tcgtgacacc ctnaac 416
```

<210> 309

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(426)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 309

```
gaactcatca tcgaggacga catcaggccc gagaagcaga agaggaagcc tgggctgcgg 60
cggaccatt caagaaagtc cggaagtctc tggctcttga cattgtggat gaggatatga 120
agctgatgat gtccacactg cccaagtctc tatccttgcc gacaactgcc cttcaaact 180
cttccagcct caccctgtca ggtatcaaag aagacaacag cttgctcaac cagggcttct 240
tgcaggccaa gcccgagaag gcagcagtggt cccagaagcc ccgaagc cac ttcacgacac 300
ctgcccctat gtccagtgc tgggaagacg gtggcctgcg gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacactttt 420
cgggac 426
```

<210> 310

<211> 2627

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene
homolog-like 2 (MYBL2) gene.

```

<400> 310
gctgacgcct tgcgagcgcg ccc gggggccc ggagcgggccg gagcagcccg ggtcctgacc 60
ccggcccggc tcccgcctcc ggctctgccc gcgggcgggc gagcgccgc cggtccgggc 120
cggggggatg tctcggcgga cgcgctgcga ggatctggat gagctgcact accaggacac 180
agattcagat gtgccggagc agagggatag caagtgcagg gtcaaattga cccatgagga 240
ggacgagcag ctgagggccc tggtagggca gtttgagacag caggactgga agttcctggc 300
cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360
tccagacctt gtcaaggggc catggaccaa agaggaagac caaaaagtca tgcagctggt 420
taagaagtat ggcacaaagc agtggacact gattgccaaag cacc tgaagg gccggctggg 480
gaagcagtg cgtgaacgct ggcacaacca cctcaaccct gaggtgaaga agtcttgctg 540
gaccgaggag gaggaccgca tcatctgcga ggcccacaag gtgctgggca accgctgggc 600
cgagatcgcc aagatgttgc cagggaggag agacaatgct gtgaagaatc actggaactc 660
taccatcaaa aggaagggtg ac acaggagg cttcttgagc gagtccaaag actgcaagcc 720
cccagtgtag ttgctgctgg agctcgagga caaggacggc ctccagagtg cccagccac 780
ggaaggccag ggaagtcttc tgaccaactg gccctccgtc cctcctacca taaaggagga 840
ggaaaacagt gaggaggaac ttgcagcagc caccacatcg aaggaacagg agcccatcg 900
tacagatctg gacgcagtgc gaacaccaga gcccttgagg gaattcccga agcgtgagga 960
ccaggaaggc tccccaccag aaacgagcct gccttacaag tgggtggtgg aggcagctaa 1020
cctcctcatc cccgctgttg gttctagcct ctctgaagcc ctggacttga tgcagtcgga 1080
cctgatgct tgggtgtgacc tgagtaaatt tgacctccct gaggaacat ctgcagagga 1140
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ccgccaagc tccgcctgg tgcccagtg gaccgagtag cgcctggatg gccacaccat 1260
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cttctggaac aaacaggaca cattggagct ggagagcccc tcgctgacat ccac cccagt 1560
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gaaacatgct gcgtttgtaa cccagatca gaagtactcc atggacaaca ctcccacac 1680
gccaaccgc ttcaagaacg cctggagaa gtacggaccc ctgaagccc tgccacagac 1740
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gatgtccaca ctgcccaagt ctctatcctt gccgacaact gcccttcaa actcttcag 1980
cctcacccctg tcaggtatca aagaagacaa cagcttgctc aaccagggt tcttgaggc 2040
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caccagcccc tccccagact ctgaggtgga ggcaacaggg ccatgtgctg cctgttgcc 2400
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gttccctccc caaggccaca gggagctccg tcagcttctc ccaagcccac gtcaggcctg 2520
gcctcatctc agaccctgct taggatgggg gatgtggcca ggggtgctcc tgtgctcacc 2580
ctctcttggg gcattttttt ggaagaataa aattgcctct ctctttg 2627

```

<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth factor, beta receptor iii (betaglycan, 300kd)

202/292

(TGFB3) gene.

<400> 311

```
cccagactca aggagttggt aaagggttaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaaatgctt tgaggctttc 120
taagcgatcc tcctgtctaa ttgtcacctt tgtctggatg cacacttctg accttgctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcaccct 240
gacaagtgtt aaggcaacat tcctttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt ccatacttg catacaccac tggcaaaatg tcttaatggc 360
aaattttgta tttcttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggccatt tc 442
```

<210> 312

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. transforming growth
factor, beta receptor iii (betaglycan, 300kd)
(TGFB3) gene.

<400> 312

```
taacaaggag gtatcactga gcttatttta gctgcaaagt ggcacatcat tattccattt 60
aatgaaattc acctcaagcc ctttttgaca tattaaatat atgggatata tttaa ggcaa 120
gagaagtaag gcaatccaaa tgagtgcct tttccaatct cagcactgtc ttgngnga 180
tggtgacact attcagataa ccaactggag accgacagat ttgccatgca tttgcatctt 240
gctagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta 315
```

<210> 313

<211> 4208

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4208)

<223> transforming growth factor, beta receptor
iii (betaglycan, 300kd) (TGFB3) gene.

<400> 313

```
tctttaagat ttgtagctac taagaaagaa aggagctttt tttccttggg ccttcaaact 60
gaaagaaccg catgagcctg acggcgcctg gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
gcaaggacac aacatcagag ggacggcaga gaatccttgt gtgtagtctt tgggtggcagt 240
ttgaaaattg caaggaggga ctttaagact acttctgatt tgcaaagatg gtctgtgctc 300
cgagcaggct aaagtgactg gacgagacgc actgttgagg aaataaaaaat gacttcccat 360
tatgtgattg ccacttttgc cctgatgagc tctgttttag oca ctgcagg tccagagcct 420
ggtgcactgt gtgaactgtc acctgtcagt gcoctccatc ctgtccaggc cttgatggag 480
agcttcactg ttttgtcagg ctgtgocago agaggcacia ctgggctgcc acaggagggtg 540
```

203/292

```

catgtcctga atctcgcact gcgccagggg cctggccagc tacagagaga ggtcacactt 600
cacctgaatc ccattctcctc a gtccacatc caccacaagt ctgtttgtgtt cctgctcaac 660
tccccacacc ccctgggtgtg gcatctgaag acagagagac ttgccactgg ggtctccaga 720
ctgttttttg tgtctgaggg ttctgtgggt cagttttcat cagcaaaactt ctccttgaca 780
gcagaaacag aagaaaggaa cttcccccat ggaaatgaac atctgttaaa ttgggcccga 840
aaagagtatg gagcagttac ttcatctacc gaactcaaga tagcaagaaa catttatatt 900
aaagtggggg aagatcaagt gttccctcca aagtgcacaa tagggaagaa ttttctctca 960
ctcaattacc ttgttgagta ctttcaaccc aaagcagcag aagggtgtgt gatgtccagc 1020
cagccccaga atgaggaagt acacatcatt gagctaattc cccccaactc taacccttac 1080
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gtcaaaaaatc tcatcctgat cttgaagtgc aaaaagtctg tcaactgggt gatcaaatct 1200
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cctgtggcaa tagtatttca tcttcggctt gaaaataatg aggagatggg agatgaggaa 1440
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cagaaccgcg ccattcgggg aggggaaggc caaaatggag gccttccgtt tcctttccca 1560
gatattttca ggagagtctg gaatgaagag ggagaagatg ggctccctcg gccaaaggac 1620
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agcgtggata ttgccctgtc tgtcaaatg t gacaatgaga agatgatcgt ggctgtagaa 1740
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agtgtcacca attccacaa gacagtgtg agattggaat gggcactcat ttggattgcc 4080
ttacttctct tgccttaaat atatccata tatttaatat gtcaaaaagg gcttgagggt 4140
aatttcatta aatggaataa tatgatgcca ctttgcagct aaaataagct cagtgatacc 4200

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tccttggt

4208

<210> 314
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 3' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 314
tnnttttttt tttncacctt tccctaatac ttnatnggtn acctctaggc ctgtgtgctg 60
ctgggtgggc ttgggggagg gcgtcactat tcagcttota ggtggaggca tgagaaggcc 120
ttggctaggc cctccagggt cccatactgt ggagtttgga ggggcaggctc tggcctttcc 180
tgggtcagca tagggcaccc aggtgggggn acaggtggac acccagcaca ggcacctagg 240
caggggcaca agtcantat ccnttagcca gcctaattgt ntttgg agaa atattccttg 300
ctgtcatcca cgttgggttt aatcgtgtca ctgccagggt tccagccagc gggacaaaant 360
ttcccatgt tcgtttgtgt attggaagg cctgggacca gccgcagagt tnatcccacg 420
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468

<210> 315
<211> 394
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(394)
<223> 5' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 315
acttcaaggc cacagcgggt gttgatggcg ccttcaaaga ggtga agctg tcggactaca 60
aagggaagta cgtggtcctc tttttctacc ctctggactt cacttttgtg tgccccaccg 120
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtctg 180
gcgtctcggg tggactctca gttcaccac ctggcttgga tcaacacccc ccggaagag 240
ggaggcttgg gccccctgaa catc ccctg cttgctgacg tgaccagacg cttgtctgag 300
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360
gggcaagggt gttcctttcg ccagatcaat gtta 394

<210> 316
<211> 937
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>

205/292

<221> misc_feature
<222> (1)..(937)
<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316
cgcgggcccca gggctcactt ggcgctgaga acgcggggtgc agcgtgtgat cgtccgtgcg 60
tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaagc 120
cagcccctga cttcaaggcc acagcgggtg ttgatggcgc cttcaaagag gtgaagctgt 180
cggactacaa agggaagtac gtggctcctt ttttctaccc tctggacttc acttttgtgt 240
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300
aagtgtctggg cgtctcggtg gactc tcagt tcaccacact ggcttggatc aacaccccc 360
ggaaagaggg aggcttgggc cccttgaaca tccccctgct tgctgacgtg accagacgt 420
tgtctgagga ttacggcgtg ctgaaaaacg atgagggcac tgcttacagg gccctcttta 480
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ccgtggatga ggctctgcgg ctggctccagg ccttccagta cacagacgag catggggaag 600
tttgtccggc tgcttgggaag cctggacgtg acacgattaa gccgaacgtg gatgacagca 660
aggaatatatt ctccaaacac aattaggctg gctaacggat agtgagcttg tgcccctgcc 720
taggtgcctg tgctgggtgt ccacctgtgc cccacctgg gtgcc ctatg ctgaccag 780
aaaggccaga cctgcccctc caaatccac agtatgggac cctggagggc tagcaaggcc 840
ttctcatgcc tccacctaga agctgaatag tgacgccctc cccaagccc accagccgc 900
acacaggcct agaggtaacc aataaagtat tagggcc 937

<210> 317
<211> 451
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(451)
<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317
gctagcacca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60
ggcccagtggt ctctgagaca gcccgctccg tgccagacat ggacctatct gggtccttct 120
atgcagcaga ctgggagcct ctgcacagtg gctccctggg gatggggccc atggcacagn 180
agctggagcc cctgtgcact ccggtgggtc cctgtactcc cagctgcact gctta cacgt 240
cttccttcgt cttcacctac cccgaggtcg actncttccc cagctgtgca gctgcccacc 300
gcaaggcagc agcagcaatg agccttctc tgactcgttc agctnaccca cgggtgctggc 360
cctgtgaggg ggcaggggaa ggggagggcag ncggcaacna caagttgcca ttgtccgagt 420
tngttgattt anagagagga gaaacaaatt t 451

<210> 318
<211> 2084
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2084)
<223> v-fos fbj murine osteosarcoma viral oncogene
homolog (FOS) gene.


```

<400> 318
aaccgcatct gcagcgagca actgagaagc caagactgag ccggcgggccg cggcgcgagcg 60
aacgagcagt gaccgtgctc ctaccagct ctgcttcaca gcgcccacct gtctccgccc 120
ctcggccctt cgcccggtt tgcctaaccg ccacgatgat gttctcgggc ttcaacgcag 180
actacgaggc gtcata ctcc cgctgcagca gcgctcccc ggccggggat agcctctctt 240
actaccactc acccgagac tcttcttcca gcatgggctc gcctgtcaac gcgcaggact 300
tctgcacgga cctggccgtc tccagtgcc acttcattcc caggtgact gccatctcga 360
ccagtcgga cctgcagtgg ctgggtgcagc ccgcccctgt ctctctgtg gcccatac gc 420
agaccagagc ccctcaccct ttccgagtc ccgccccctc cgctggggct tactccaggg 480
ctggcggtgt gaagaccatg acaggaggcc gagcgagag cattggcagg aggggcaagg 540
tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaagggaa aggaataaga 600
tggctgcagc caaatgccgc aaccggagga gggagc tgac tgatacactc caagcggaga 660
cagaccaact agaagatgag aagtctgctt tgcagagcga gattgccaac ctgctgaagg 720
agaaggaaaa actagagttc atcctggcag ctcaaccgac tgcttgcaag atccctgatg 780
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gttactgatc atgcattgtt gaggtggtct gaatgttctg acattaacag ttttccatga 1920
aaacgtttta ttgtgttt tt aatttattta ttaagatgga ttctcagata tttatatattt 1980
tattttattt ttttctacct tgaggtcttt tgacatgtgg aaagtgaatt tgaatgaaaa 2040
atttaagcat tgtttgctta ttgttccaag acattgtcaa taaa 2084

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<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 319

```

ctgcaaagcc aatcaagaag tgttggaagg aaaaagtgtg aaagttatto ttgcatattt 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangcaa cattcttctc 180
ttccctaata gctacaatnt gatacagtag gcaacagctc acttgaaagt gctagantca 240

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<210> 320

207/292

<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 320
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agaatacacc gtttctatat gacctggtta tgacccatgc tcttcagtgg cccagtctta 120
ccgttcagtg gcttcctgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 240
ttcccaatga tgatgcacag tttgat gctt cccattgtga cagtgacaag ggtgaatttg 300
gtggctttgg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaagga 360
gaagttaaac cgtgctcggt aacatggcgc cagantcctt cacatccatt gcttacaaan 420
acaccctctt gcttgatggt gttggnnttt tgactat 457

<210> 321
<211> 1946
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1946)
<223> retinoblastoma -binding protein 7 (RBBP7)
gene.

<400> 321
gcctcgtcag ctgcctgggc gggc tgggag gcgcgggttg aaaagtctcg ttccaagttt 60
ggagagagag agaagagcgc ctacagacctc ggtaccgcgc agcggggagg aggcaggaaa 120
gaaggacgcg gcgtctgggg agcaccacag cagcaagacg gggcccgggc ttctcgacagt 180
ggggagtgtg acgcgcttg gaaaggcagg agcgcacagc gtcgggctgc tcttggtctaa 240
cgagaggagt ccgagggcgc ggcgaggggc gaacgaccgc acgcaagatg gcgagtaaag 300
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataataa atctggaaga 360
agaatacacc gtttctatat gacctggtta tgacccatgc tcttcagtgg cccagtctta 420
ccgttcagtg gcttcctgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 540
ttcccaatga tgatgcacag tttgatgctt cccattgtga cagtgacaag ggtgaatttg 600
gtggctttgg ttctgtaaca ggaataattg aatgtgaaat taaaatcaat cacgaaggag 660
aagtaaaccg tgctcggtac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720
cttctgatgt gttggttttt gactatacaa aacaccctgc taaaccagac ccaagtggag 780
aatgtaatcc tgatctcaga ttaagaggtc accagaagga aggcctatggt ctctcctgga 840
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aatattattc agccaccggc tctgcggata agaccgtagc tttatgggat ctgcgtaact 1200
taaaattaaa actccatacc ttcgaatctc ataaagatga aattttccag gtccactggg 1260
ctccacataa tgaaactatt ctggcttcaa gtggtactga ccgcgcctg aatgtgtggg 1320

208/292

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atttaagtaa aattgg ggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
tcctgtttat tcatggagga cacactgcta agatttcaga ttttagctgg aaccccaatg 1440
agccttggtt catttgctca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaaatattt caatgatgaa gagtcagatg tcacgacatc cgaactggag ggaca aggat 1560
cttaaaccct aagtacgaga aatgtttctg ttgaatgtaa tgctacatga atgcttgatt 1620
tatcaagcgc caaaaaggca ttgtatagta ggaaatgtaa gtgggggtggc ttatggcttc 1680
tttatcctct gattctagca ctttcaagtg agctgttgcg tactgtatca tattgtagct 1740
attagggaag agaagaatgt tgcttaagaa agaacatcac cattgatttt aaatacaagt 1800
agcagggtat tgcctttgat tcaactgttt taagtcttca ttttctcaaa ctaagtgcct 1860
gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaat 1946

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<210> 322

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 322

```

tatagaaatt ctttattatt a gacaaaaat agactctctt ttttccccta ttcattgtgat 60
cctactctga atctctgctc agaggaggca gtgactcgct cccacccct ctccatccc 120
tgccgtgctg gcacctgcag ctgggtggaa ctggcagggg ctgatccct gggagggtg 180
acgttctcct gcagggtggg ctgctgctgc tccttcgggg ctcaactgct gatgcctct 240
caccctcac acaccatct ctgccatctg ctccatggc aagggtcatc ttgtggggcc 300
tggtccactt taacttaggc agggctgggg ggcgggggaa gggagaggca gtgttccag 360
gggcc 365

```

<210> 323

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 323

```

tcaagggctg cccagtgag ccctactttg gcagcctgtc cgccttggtc tcccagcact 60
ccatctcccc catctccctg ccctgctgcc tgcgcattcc cagcaaagat cctctggaag 120
agaccccaga ggctccagt cccaccaaca tgagcacagc gncagacctc ctgcgtcagg 180
gtgctgcctg caggtngctc tacttgacct cagtggagac agagtcaactg acgggcccc 240
aagctgtggc ccgggccagc tctgcagctc tgagctgta g ccccgcccg acaccagctg 300
ttgtccactt caaggtgtca gccagggca ttacactga cgggacaacc aaaggaagct 360
ctttnttttc gccgccatta tccagtggaa cagcatcacc 400

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209/292

<210> 324
 <211> 489
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(489)
 <223> 5' terminal sequence. atp-binding cassette,
 sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324
 ntctggcaca gnaagataca actctgtgct gaacagctgc tgcctgaggc tgacctggcc 60
 attcttccca gcagcgacct gacggagatt ggagagcgag tancaacctg agcgggtgggc 120
 agcgcagagg atcagccttg cccgggcctt gtatagtgcac aggagcatct acatcctgga 180
 cgaccccctc agtgccttag atgcccattgt ggaanccaca tncctcaata gtgctatccg 240
 gaaacatctc aagtccaaga cagttctgtt tgttaccac cagt tacagt acctgggttg 300
 actgtgatga agtgatcttc atgaaagagg gctgtattta cgggaaagag ggcacccttg 360
 gagggaantg atggatttta aatgggtgatt atggttacct ttttaattaa cntgttggtg 420
 ggggagagac accgccattg agntcatttc aaaaagggga accgtnggtt cacagaggag 480
 ttcacagtt 489

<210> 325
 <211> 5838
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5838)
 <223> atp-binding cassette, sub-family c
 (cftr/mrp), member 5 (ABCC5) gene.

<400> 325
 ccgggcaggt ggctcatgct cgggagcgtg gttgagcggc tggcgcgggtt gtccctggagc 60
 aggggcgcag gaattctgat gtgaaactaa cagtctgtga gccctggaac ctccgctcag 120
 agaagatgaa ggatatcgac ataggaaaag agtatatcat cccagtcct gggtatagaa 180
 gtgtgaggga gagaaccagc acttctggga cgcacagaga ccgtgaagat tccaagttca 240
 ggagaactcg accgttgga tgccaagatg ccttggaac agcagcccga gccgagggcc 300
 tctctcttga tgcctccatg cattctcagc tcagaatcct ggatgaggag catcccaagg 360
 gaaagtacca tcatggcttg agtgctctga agcccatccg ga ctacttcc aaacaccagc 420
 acccagtga caatgctggg cttttttcct gtatgacttt ttogtggctt tcttctctgg 480
 cccgtgtggc ccacaagaag ggggagctct caatggaaga cgtgtggtct ctgtccaagc 540
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 tcatcctgtc catcgtgtgc ctgatgatca cgcagctggc tggcttcagt ggaccagcct 720
 tcatggtgaa acacctcttg gagtataccc aggaacaga gtctaacctg cagtacagct 780
 tgttgtagt gctgggcctc ctccctgacgg aaatcgtgcg gtcttggtcg cttgcaactga 84 05
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tctatatata	attctgtaca	tagcctatat	tataagttaa	aatgtaagct	gtttatttta	4800
tattaaaata	agcactgtgc	taataacagt	gcataatcct	ttctatcatt	tttgtacagt	4860

211/292

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ttgctgtact agagatctgg ttttgctatt agactgtagg aagagtagca tttcattcctt 4920
ctctagctgg tggtttcacg gtgccaggtt ttc tgggtgt ccaaaggaag acgtgtggca 4980
atagtgggccc ctccgacagc cccctctgcc gcctccccac agccgctcca ggggtggctg 5040
gagacgggtg ggcggctgga gaccatgcag agcgccgtga gttctcaggg ctccctgcctt 5100
ctgtcctgggt gtcacttact gtttctgtca ggagagcagc ggggcgaagc ccaggccccct 5160
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gttggttcca agccctggag ccaactgctg ctttttgagg tggcact ttt tcatttgcct 5400
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ctcaccgcag tcgtgcaca gtctctctct ctctctcccc tcaaagtctg caactttaag 5520
cagctcttgc taatcagtgt ctcacactgg cgtagaagtt tttgtactgt aaagagacct 5580
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atgtcgtgac caactagaca ttctgtcgcc tttagcatgtt tgctgaacac cttgtggaag 5760
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aaaaaaaaa aaaaaaaaaa 5838

```

<210> 326

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 326

```

aanganatat taacaaaatt gtttaataaaa atttataaaa atgcatcttt gagaatactt 60
tntcagctt gaattgtttt ccttttccac ccccaaagaa aatacacaat tatcagcacc 120
cacacatgta tacactcaaa actacagtga catt ctctac acagnnctat attcgatata 180
gcttgaactg ccgaaaaatc angacaattc caaaagggtga ttgcagggtt gatttttttc 240
tccaaaacac ttgaganaca gtaaagctat ttcaacaaag gtcttttntt tgattgtcaa 300
aggttgaaat tcacatttna ntannagggg ntccnaatca ngntcctcac taccctctac 360
ccctcancta accccctttg ggcc 385

```

<210> 327

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(423)

<223> 5' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 327

```

ggcacgagca aganaggagt tctctgatgc agaaattatt gggctctttt agggtaagaa 60
gtttgtgtct ttgtctggcc acatcttgac taggtattgt ctactctgaa gacctttaat 120
ggcttccctc tttcatctcc tgagtatgta acttgcaatg ggcagctatc c agtgacttg 180

```

212/292

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ttctgagtaa gtgtgttcat taatgtttat ttagctctga agcaagagt atatactcca 240
gggacttaga atagtgccta aagtgtctga gccaaagaca gagcggaaact atgaaaagt 300
ggcttggaga tggcaggaga gcttgtcatt gagcctgggc aatttnagca aactgatgtc 360
tgaggatgat tcgaggtggg tcttacctca tctactgnaa aattctggta aggaatggga 420
ggg

```

<210> 328

<211> 4828

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)
(CDH1) gene.

<400> 328

```

agtggcgtcg gaactgcaaa gcacctgtga gcttgccgaa gtcagttcag actccagccc 60
gctccagccc ggcccgaccc gaccgcaccc ggccgctgcc ctgcctcggc gtccccggcc 120
agccatgggc ccttgagacc gcagcctctc ggccgtgctg ctgctgctgc aggtctcctc 180
ttggctctgc caggagccgg agccctgcca ccctggcttt gacgccgaga gctacacgtt 240
cacggtgccc cggcgccacc tggagagagg ccgcgtcctg ggcagagtga attttgaaga 300
ttgcaccggt cgacaaagga cagcctattt ttccctcgac acccgattca aagtgggac 3 60
agatggtgtg attacagtca aaaggcctct acggtttcat aaccacaga tccatttctt 420
ggtctacgcc tgggactcca cctacagaaa gttttccacc aaagtcacgc tgaatacagt 480
ggggcaccac caccgcccc cgccccatca ggcctccgtt tctggaatcc aagcagaatt 540
gctcacatatt cccaactcct ctctggcct cagaagacag aagagagact gggttattcc 600
tcccatcagc tgcccagaaa atgaaaaagg ccattttcct aaaaacctgg ttcagatcaa 660
atccaacaaa gacaaagaag gcaaggtttt ctacagcatc actggccaag gagctgacac 720
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gaatgcagtt gaggatccaa tggagatttt gatcacggtg accgatcaga atgacaacaa 900
gcccgaattc acccaggagg tctttaaggg gtctgtcatg gaaggtgctc ttccaggaa 960
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taacaggaac acaggagtca tcagtgtggt caccactggg ctggaccgag agagtttccc 1140
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ggtgggtgac tacaaaatca atctcaagct catggataac cagaataaag accaagtgcac 2160
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gcccttactg cccccagagg atgacacccg ggacaacggt tattactatg atgaagaagg 2400
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attttgtaa accataaaaa aaaaaaaa 4828

```

<210> 329

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 5' terminal sequence. zinc finger protein
144 (mel-18) (ZNF144) gene.

<400> 329

```

attcggcaca tgattccact tccgtttccc agggcaacgc tccccagtc cccaccc cc 60
gaccccgaa tcatgcatcg gactaacagg atcaaaatca cagagctgaa cccccacctc 120

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atgtgtgccc tctgcggggg gtacttcacg gacgccacca ctatcgtgga gtgcctgcat 180
tccttctgca aaacctgcat cgtgcgctac ctggagacca acaaatactg ccccatgtgt 240
gacgtgcagg tccataaaac ccggccgctg ctgagca ttc aggtctgaca aaacatttca 300
agacattgtc ttacaaattg gtccctgggg ctttttaaag atggagattg aaacgggcgg 360
cgggatttct tatggcaggc gttaccctt ggacgggagg ttcccccaac ggnttccaat 420
tgagggaccg ngggcgaggg tttttnggga ggcagggaga aggggggttt t 471

```

<210> 330

<211> 2227

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)
gene.

<400> 330

```

gagagcccga acaggaagag ggtacagctt tgtg caggtc acatgcccac tgcagccctc 60
cagcctctgg tccccagagc ggacttttga agctgaactg cttttgttgc tggaaagactt 120
atgttataat ttaccttggg tggaccaggg tcgtacaaaa gggcaacgct cccagctccc 180
cccactcccg accccggaat catgcatcgg actacacgga tcaaaatcac agagctgaac 240
cccacctca tgtgtgccct ctgcgggggg tacttcatcg acgccaccac tatcgtggag 300
tgctgtcatt ctttctgcaa aacctgcac gtgcgctacc tggagaccaa caaatactgc 360
cccatgtgtg acgtgcaggc ccataaaacc cggccgctgc tgagcatcag gtctgacaaa 420
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cggcgggatt tctatgcagc gtacccctg acggagggtc ccaacggctc caatgaggac 540
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acactcg 2227

```

<210> 331
<211> 254
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(254)
<223> 3' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331
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ggcatcaagg ctgggctaac ccagtctcat gaccttgtga atccagtcca caaacacaga 120
gacacgcgtg aagacagctg gccagcggga ccttgccgat actcgggttg ggattataat 180
tccttcacagg gacccagcag ttgtgggtaa agcaggcaag tgggcccccg tagtcaccct 240
cacaggcccc caca 254

<210> 332
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(362)
<223> 5' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332
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acgtgcgct gatgaccagc cgccatcaat cctggacccc ccagaccagg tgcagtttga 120
gaagtgtggc aagaggggtg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180
ggccatccgg gcaactcacc ctggacagtc agcttgcgga atcggcaggg ccagcatttc 240
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ag 362

<210> 333
<211> 2219
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2219)
<223> macrophage stimulating 1 (hepatocyte growth
factor-like) (MST1) gene.

216/292

<400> 333

```

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gctacatgcg gtggtgcccc ggccttggca ggaggatgtg gcagatgctg aagagtgtgc 180
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gttcccgaat gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg 480
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<210> 334

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 334

```

gaaaggaagg caaactctgc ccccc gctca gagtcccccc aaccctcaact gtttcccggt 60
gccattgatg gggagggttca cgtactcagg ggaggccagg naggcntgna gcttggggccg 120
ggcactgagg cgccccacat atgctgagag caggggggaac gcatccaggc agccagggt 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctgggt ctgggacagc agggctctcaa aaggcttcag 300

```

217/292

```
ttgccccgggc agtgccttca catagtcac cttgccccgcc tcatagttgg tntagatgag 360
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggctg 420
nctccntttt t 431
```

<210> 335
<211> 305
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(305)
<223> 5' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

```
<400> 335
nattcggcac aggtcgccac catgccgccc tacaccgtgg tctatttccc agttcgaggc 60
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180
aagttccagg acggagacct naccctgtac cagt ccaata ccctcctgcg tcacctgggc 240
cgcaccttg ggcctnctatg ggaaggacca gcaggangca gccctgggtg acatngtgaa 300
tgacg 305
```

<210> 336
<211> 737
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(737)
<223> glutathione s-transferase pi (GSTP1) gene.

```
<400> 336
ggagtttcgc cgccgcagtc ttgccacca tgccgcccta caccgtggtc tatttcccag 60
ttcgaggccg ctgcgcggcc ctgcgcagtc tgctggcaga tcagg gccag agctggaagg 120
aggaggtggg gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatac 180
ggcagctccc caagttccag gacggagacc tcacctgta ccagtccaat accatcctgc 240
gtcacctggg ccgcaccctt gggctctatg ggaaggacca gcaggaggca gccctgggtg 300
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420
agaccctgct gtcccagaac cagggaggca agaccttcat tgtgggagac cagatctcct 480
tcgctgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540
tggatgcgtt cccctgctc tcagcatatg tggggcgcc cagcgccgg cccaagctca 600
aggccttccct ggctccctc gagtacgtga acctcccat caatggcaac gggaaacagt 660
gagggttggg gggactctga gcgggaggca gagtttgctt tcttttctcc aggaccaata 720
aaatttctaa gagagct 737
```

<210> 337
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(372)
<223> 3' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 337
gtgggnctgt gttgaaacag gccacgtaaa gcaactctct aaaggtcaaa ccaccataga 60
tttgaatctg ctggtcattc gccatctgga tttttaactg aatgaatctc atgggtttta 120
ccaaacatgc atgtaatcct gaataccatg anttaaagtc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtgaca 300
tcnngggttt ttcttagggg aggctgagga ctgaggggct tatctcacct tctcaggaat 360
gctttttgaa gg 372

<210> 338
<211> 508
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(508)
<223> 5' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 338
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tcagttacct taaaccctga ttgtgtatat tcatatatat tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatcctct ggaacttgag 180
gaagtgaaca tttcggtgac ttccgcatca ggaaggctag agttaccag agcatcaggc 240
cgccacaagt gcctgctttt aggagaccga agtccgcaga acctgcctgt gtcccagctt 300
ggaggcctgg gtccctggga ctgagccggg gccctcactg gccttccttc caggggatgg 360
atcaacaggg gcagtggtgt cttccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttagggggg tttgggtggg gcttgttcac ctgg gggggc 480
ttccaggtag ggcccttttt aagtggga 508

<210> 339
<211> 445
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(445)
<223> 3' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 339

219/292

```

tttttttant caaaagtttg aaattcaagt aactttatit aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctagggttaa ctagaccaga tctgactt tg gactttatct tttaaacaan 180
ttgcagagan tagagaaaaa antagggttat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttggttga cagaaaagac ttcaggtata tgctgggcàt cttaggaagn 300
cagttctcaa agggnccttag gttttatttn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgn tctt ggggngggcc aggtaggtn tttagggtgc ccntatccc 420
ganttttata ctctncaccg ggggg 445

```

<210> 340

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 5' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 340

```

gctccagcgt tgtaaacctg cagagatgga ctcgctccac gtctcttttg tgcagctcac 60
cctgcgggtct gagggcttcg acacctaccg ctgcgaccgc aacctggcca tgggggtgaac 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcggatac cttggcgcta gtatttgaag caccaaacca ggagaaagt 240
tcagactatg aaatgaagtt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgccntct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact 437

```

<210> 341

<211> 1231

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)
gene.

<400> 341

```

aggctctcagc cggctcgtcgc gacgttcgcc cgctcgtctt gaggtccctg aagccgaaac 60
tagctagact ttcctccttc ccgcctgcct gtagcggcgt tgttgccact ccgccaccat 120
gttcgaggcg cgctcgttcc agggctccat cctcaagaag gtgttgagg cactcaagga 180
cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240
ctcgtccac gtctcttttg tgcagctcac cctgcggctc gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaaa tactaaaatg 360
cgccggcaat gaagatatca ttactactaag ggccgaagat aacgcggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgga ttccagaaca ggagtagcgc tgtgtagtaa agatgccttc 540
tggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660

```

220/292

```

attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc tttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc cttgtttag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatttgta cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa cctagaagta tttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaatttaaat aaagttactt gaatttcaaa c 1231

```

<210> 342

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 3' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 342

```

tttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccogtgt 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatatatt c cacaattact tgctctcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aagggttaagt gttctcggtt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggaggggaac gatgatgcca agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtactttttt tac 383

```

<210> 343

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 343

```

gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcatct ttgtcctaac atgagtgctt gtaacaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg tttaatgctt cccttccctt cccacataac atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gttttagagt aatgggggtc ttgcctaatt gaactccatc actgtacaca 360
gaatgaagga nttaatgccg tgtaattttt cttgttattt aagg atgccg tggatttggt 420
aaaagggtctg gtattttgctg gggatgtctg gggttaggga ggccttacc ataggggntg 480
ggg 483

```

<210> 344
 <211> 2722
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2722)
 <223> adenovirus 5 ela binding protein (BS69)
 gene.

<400> 344
 ggagcataat gctaaagaag taaacaggtc atggcacggt taacaaaaag acgacaggcg 60
 atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120
 ttgccaaatc tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggt 180
 gattttttaca tcattacaca gatatgtcat tttcattagt tgtatcattg ttataaactg 240
 gtatatgtct cgagtccacg gtatgcaccc taaagagacc acccgtcagc tgagcttagc 300
 tgtgaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaagggt caaaagctgg 360
 tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaaatca 420
 tgactgggat tgttttgaat gccattttgcc tggagagggt ttgatatgtg acctgtgttt 480
 tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540
 ctggcagtgcc ccagttttgca ggagcattaa gaagaagaat acaaacaaac aggagatggg 600
 cacatacctc agattcattg tctcccgcat gaaggagagg gctatagatc ttaataaaaa 660
 ggggaaggac aataaacacc cgatgtacag gaggctgggt cactcagctg tggacgttcc 720
 caccattcaa gagaaagtga atgaagggaa ataccgaagt ta tgaagagt tcaaagctga 780
 tgcccaattg cttctccaca ataccgtgat tttctatgga gcagacagtg agcaagctga 840
 cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900
 gaattgcttt tacttgtcaa atgctcgtcc tgacaactgg ttctgttatc cttgtatacc 960
 taatcatgag ctggttttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020
 gcagaaaagaa gacaatcaag tcgacgttcg cttctttggc caccaccacc agagggcctg 1080
 gattccttct gaaaacattc aagatatcac agtcaacatt catcggtcgc acgtgaagcg 1140
 cagtatgggt tggaaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200
 agggagattt tggaaatcta agaattgagga ccgaggtgag gaagaggcag aatccagtat 1260
 ctctccacc agtaatgagc agctaaaggc cactcaagaa ccaagagcaa agaaaggacg 1320
 acgtaatcaa agtgtggagc caaaaaagga agaaccagag cctgaaacag aagcagtaag 1380
 ttctagccag gaaataccca cgatgcctca gccc atcgaa aaagtctccg tgtcaactca 1440
 gacaaaagaa ttaagtgcct cttcaccgaat aatgtctgat cggagcacc agaccacaaa 1500
 cgacggcgtg tgtcagagca tgtgccatga caaatcaccc aagatcttca atgacttcaa 1560
 agaccgtagt aagtcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620
 gaagctgcgt tctgaaatgg aagaagaaaa gagacaagct gtaataaaag ctgtagccaa 1680
 catgcagggt gagatggaca gaaaatgtaa gcaagtaaag gaaaagtgtg aggagggaatt 1740
 tgtagaagaa atcaagaagc tggcaacaca gcacaagcaa ctgatttctc agaccaagaa 1800
 gaagcagtggt tgctacaact gtgaggagga ggccatgtac cactgctg ct ggaacacatc 1860
 ctactgctcc atcaagtgc agcaggagca ctggcacgcg gagcacaagc gcacctgccg 1920
 ccgaaaaaga tgaagctggc ctttcccgga gtcaccccgga tgattactct tttcagacac 1980
 agcggttttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag 2040
 ctttaaaaca cttttcgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100
 ctccgaagtt tttcagggg taaaagtaac atcagtggag ggtattattt taaataaatt 2160
 ttaattgaga atttgttgca ttttcagcaa atttttaaac atttttaggt tttacagaga 2220
 ttttaacctt taaacaacag atcttttaaaa aacagggtgaa tacaagttag ttttaacaaag 2 280
 aaacatttag aatagatctg aatgtaagaa ctacagaact gtttcagaaa taaaacatac 2340
 taccttgatg tgacattttt ttcttaacct tgttgagctg gttttgttca gcttaattta 2400
 ctgttcaaa gcatatctg ttggtcacac cagtgggtat atgattgaat ttagggaaca 2460
 gggttgacac agcagggtc gtccctgcata tttttt ctta aatattttcc aattgtgttt 2520
 ttcatattt cttttcaata tataactttt ataacaaatt attagctttg atctttagt 2580
 ttaaaattgc agggaaactg ggtaatcttt tactgagctg gatcttagag aaaatgaata 2640
 tttaaatttt aaagtttgcc acatttcatc tttgtcctaa catgagtgct tgtaacaaaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

<210> 345

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. matrix

metalloproteinase 11 (stromelysin 3) (MMP11) gene.

<400> 345

```
gcatgcagca tcctgagtgg tagcgtcgat ctcagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgccg ggtgctgggg tggaaacgcc agtagtccct 120
gcctcggaag aagtagatct tggtcttctc gggaccccag accaaggc ag catggaccgg 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggactgg cttttcaccg 240
tcgtacacc agtacttgag caccttggga agaaccaaat gtggggcccg cttaccacgc 300
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaattttgg 360
gca
```

<210> 346

<211> 2260

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2260)

<223> matrix metalloproteinase 11 (stromelysin 3)

(MMP11) gene.

<400> 346

```
aagcccagca gccccggggc ggatggctcc ggccgcctgg ctccgcagcg cggccgcgcg 60
cgccctcctg ccccgatgc tgetgctgct gctccagccg ccgcgcgtgc tggcccgggc 120
tctgccgccg gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agccctgccc agtag cccgg cacctgcccc tgccacgcag gaagcccccc ggccctgccag 240
cagcctcagg cctccccgct gtggcgtgcc cgaccatct gatgggctga gtgcccgcaa 300
ccgacagaag aggttcgtgc tttctggcgg gcgctggggag aagacggacc tcacctacag 360
gatccttcgg ttcccatggc agttggtgca ggagcaggtg cggcagacga tggcaga ggc 420
cctaaaggta tggagcgatg tgacgccact cacccttact gaggtgcacg agggccgtgc 480
tgacatcatg atcgacttcg ccaggctactg gcatggggac gacctgccgt ttgatgggcc 540
tgggggcatc ctggcccatg ccttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcagggtggc 660
agcccatgaa tttggccacg tgctggggct gcagcacaca acagcagcca aggccctgat 720
gtccgccttc tacacctttc gctaccact gagtctcagc ccagatgact gcaggggcgt 780
tcaacaccta tatggccagc cctggcccac tgtaacctcc aggaccccag ccctggggcc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgaggcc tcctttgacg cggctctccac catccgaggc gagctctttt tcttcaaagc 960
gggctttgtg tggcgccctc gtggggggca gctgcagccc ggctacccag cattggcctc 1020
tcgcacttg ccaggactgc ccagccctgt ggacgctgcc ttcgaggatg ccca gggcca 1080
catttggttc ttccaagggt ctcagtactg ggtgtacgac ggtgaaaagc cagtcctggg 1140
```

223/292

```

ccccgcaccc ctcaccgagc tgggcctggt gaggttcccg gtccatgctg ccttgggtctg 1200
gggtcccagc aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccgag cgtgtagaca gtcccgtgc c ccgcagggcc actgactgga gaggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc cccgtctcgt 1440
gggtcctgac ttctttggct gtgccgagcc tgccaacact ttctcttgac catggcttgg 1500
atgccctcag gggtgctgac cctgccagg ccacgaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtggggtag aaccaccatg acaactgccg ggagggccac gcaggctcgtg gtcacctgcc 1680
agcactgtc tcagactggg cagggaggct ttggcatgac tt aagaggaa gggcagtctt 1740
gggaccgct atgcaggctc tggcaaacct ggctgccctg tctcatccct gtccctcagg 1800
gtagcaccat ggcaggactg ggggaactgg agtgctcctt ctgtatccct gttgtgaggt 1860
tccttccagg ggctggcact gaagcaaggg tgctggggcc ccattggcctt cagccctggc 1920
tgagcaactg ggctgta ggg cagggccact tcctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc aggccaaaaa 2040
gttcacagtc aaatggggag gggtattctt catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttct cagcac tgct 2160
atcctccaaa gccattgtaa atgtgtgtac agtgtgtata aacottcttc ttcttttttt 2220
tttttaaact gaggattgtc attaaacaca gttgttttct 2260

```

<210> 347

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(273)

<223> 3' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 347

```

atgtttattg aacgtaacag tataatttcat gtagtttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcactt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaagggtg tgttacgaat 180
catcggggct gtggccagnt tgcctcacgg aggtgcagg aggtcggggc ctcactaggg 240
canctggagg agcacggact gccctgccgg cag 273

```

<210> 348

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 348

```

ggagtacaga acattgtggt aggggaaggg actcactttc tcattcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac ttgtagcaaa 120
gattacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```

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```
cctcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat cacccagagg 300
gagcttggtt tccagccngg tgaagnacca                               330
```

<210> 349
<211> 1168
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:prime r

<220>
<221> misc_feature
<222> (1)..(1168)
<223> hypothetical protein mgc13071 (MGC13071)
gene.

```
<400> 349
aaatgatgat agtagtacct acagtatagt gctgttagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcagggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtccat cggcaagttt ggcctggcct tagctgtttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcattcctt tccggcccat cactagccag cttcctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tcctcaagtc actggtggct cgctttgatg ctggagaact aatcaccagc agggagctgg 540
tcctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctattctctg 600
acgacgtgtc tttgacacat ctgaccttct tgaaggagtt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcggcc atcatctctg ctgagggtga 720
ctccaaggca gctgagctga tcgccaactc actggccact gcaggggacg gccagagcga 7 80
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtccgtgct cctccagctg ccctagttag gccccagcct 900
acctgcacct ccgtgaggca actgggccac agccccgatg attcgtaaca ccacctttcg 960
ccctaccccc agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacgtt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                               1168
```

<210> 350
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(315)
<223> 5' terminal sequence. interleukin enhancer
binding factor 2, 45kd (ILF2) gene.

```
<400> 350
ctggcttttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
cccaatcttc gaaaactgga tccagaactc catttggata tcaaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctggttc gaggaaaatg cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggacttgag gattcgtttt ccnggctttg agc cctcaca 240
```

225/292

```

ccnnggatnc ttgaactact aggnccattat gctgtgatga acaaccccac caganagcct 300
ttggcnctaa acgtt                                     315

```

```

<210> 351
<211> 1552
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(1552)
<223> interleukin enhancer binding factor 2, 45kd
      (ILF2) gene.

```

```

<400> 351
cggttggtgc ggcctccatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60
ggtcgtggtg ggcgctttgg ttccagagga ggcccaggag gag ggttcag gccctttgta 120
ccacatatcc catttgactt ctatttgtgt gaaatggcct ttccccgggt caagccagca 180
cctgatgaaa cttccttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240
tctgctgaac aggcattctat cctttctctg gtgacaaaaa taaacaatgt gattgataat 300
ctgattgtgg ctccagggac a tttgaagtg caaattgaag aagttcgaca ggtgggatcc 360
tataaaaagg ggacaaatgac tacaggacac aatgtggctg acctggtggt gataactcaag 420
attctgccaa cgttggaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480
gcacaggatc cttctgaagt ttttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540
tcttctgatg ctacagtga gattctcatt acaacagtgc caccaatct tcgaaaactg 600
gatccagaac tccatttggg tatcaaagta ttgcagagtg ccttagcagc catccgacat 660
gcccgtctgt tcgaggaaaa tgcttctcag tccacagtta aagttctcat cagactactg 720
aaggacttga ggattcggtt tcttggttt gagccctca c acctggat ccttgacctg 780
ctaggccatt atgctgtgat gaacaacccc accagacagc ctttggccct aaacgttgca 840
tacaggcgct gcttgcatg tctggctgca ggactgttcc tgccagggtc agtgggtatc 900
actgaccctt gtgagagtgg caactttaga gtacacacag tcatgaccct agaacagcag 960
gacatggtct gctatacagc tcagactctc gtccgaatcc tctcacatgg tggctttagg 1020
aagatccttg gccaggagg tgatgccagc tatcttgctt ctgaaatatc tacctgggat 1080
ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140
gaggaagaag aggagaatac agaaagaacc acctcaagga gaggaagaag aaagcatgg a 1200
aactcaggag tgacattccc ttcactcctt ttcctaccca agggaaagac tggagcctaa 1260
gctgcctgct actggcttta catggtgaca gacattccgt ggataggaag atagcaggag 1320
aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380
tttgtgacct atgccatcca tctataatgg agg atacca catttcttcc taatattcta 1440
taatctccaa ctctgaaaa cccctctctc aactaatact ttgctgttga aatggttga 1500
aatgttaagt gtctggaaat ttttttttct aagaaaaact attaaagtac tt 1552

```

```

<210> 352
<211> 396
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(396)
<223> 3' terminal sequence. hypothetical protein
      flj11307 (FLJ11307) gene.

```

226/292

<400> 352

```

ctccattaca gggttttttgc cacttgctgt gaggataggg ccctgagttc ttacctctaa 60
ggtactggag gtttc agttg tagaatttcc agtattattg cttgagtttg aagacactgt 120
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcac 180
aaagcctggt ggatatccca ttgcctgcaa taccttcacc gctacgtgaa agttttgctg 240
ttttcttgga tggctctgag gcttcataatg ttgtgccatc cacatctaca gacattg tga 300
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360
tgatctgaat taagcntcat tagtggcatt ccataa 396

```

<210> 353

<211> 1858

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307)
gene.

<400> 353

```

tcgatgaaag atcctccgga ottattggac aggcagaaat gcccgaaacgc cttggcgtct 60
cttcgacatg ccaaattggtt tcaggcaagg gcaaattgat taaaatcatg tgtaat tgtc 120
ctccgcattc tgcgtgattt gtgcaacaga gtccccacat gggcaccatt gaaaggatgg 180
ccactagaac ttatatgtga aaagtctata ggtacttgta atagaccttt gggcgctggg 240
gaggccttga gacgagtaat ggagtgtttg gcatctggaa tactacttcc tgggggtcct 300
ggtcttcatg atccttgtga gcgagaccca acag atgctc tgagctatat gaccatccag 360
caaaaagaag atattaccca cagtgcacag catgcaactc gactatcagc ctttggccag 420
atttacaagg tgctggagat ggacccctt ccacttagta agccttttca gaagtattcc 480
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540
ggattagggg atgataaaga cccaacaag aagatgaaac gaaacttaag gaaaattctg 600
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660
cttcagtata agctcctatc tcagtctggc ccggttcatg cccagtcctt cacaatgtct 720
gtagatgtgg atggcacaac atatgaagcc tcaggaccat ccaagaaaac agca aaactt 780
cacgtagcgg tgaaggattt gcaggcaatg ggatatccaa caggctttga tgcagatatt 840
gaatgtatga gttccgatga aaaatcagat aatgaaagta aaaatgaaac agtgtcttca 900
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960
actcagggcc ctatcctcac agcaagtggc aa aaacctg taatggagct caatgaaaaa 1020
agaagaggtc tcaagtatga actcatctca gagactggtg gaagccatga caagcgcttt 1080
gtaatggagg tagaagttaga tggacagaaa ttcagaggcg cagggtccaaa taagaaagtg 1140
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200
aataataaga aaaagaagat tatccctcag gcaaaggcg ttgtgaatac agctgtgtct 1260
gcagcagtc aagctgttcg gggcagagga agaggaaactc taacaagggg agcttttgtt 1320
ggggcgacag ctgctccttg ctacatagct ccaggctatg gaacaccata tggttacagc 1380
acagctgccc ctgcctatgg tttacccaag agaatggttc tgttac ccgt tatgaaattt 1440
ccaacatate ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgtcttct 1560
ttgaacacat acttgatcaa aattattttg aaagaacatc tttcctactt tttgatttta 1620
acaaatgcaa atttagttct ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680
acggtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaag 1740
tctagcagtt caaagtttaa gttttaagag acgtatcaga ttatgtaaaa ttaaatttgt 1800
gaaggatgta tagagtctca aacactgac acaataaac tgctttgttg taacacag 1858

```

<210> 354

<211> 242

<212> DNA

227/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(242)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog (MYB) gen e.

<400> 354

```

agaaccccgag ctatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacgggtcccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt                                     242

```

<210> 355

<211> 3225

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene
homolog (MYB) gene.

<400> 355

```

ggcggcagcg ccctgccgac gccggggagg gacgcaggca ggcggcgggc agcggggaggc 60
ggcaccgccg tgctccccgc ggctctcggc ggagccccgc cgcccgccgc gccatggccc 120
gaagaccccg gcacagcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
accatgacta tgatgggctg ctccccaagt ctggaaagcg tcaacttggg aaaacaagg 240
ggacccggga agaggatgaa aaactgaaga agctggtgga acagaatgga acagatgact 300
ggaaagtatt tgccaattat ctcccgaaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaaccctgag ctcatcaagg gtccttggac caaagaagaa gatcagagag 420
tgtatagagct tgtacagaaa tacgggtccga aacgttggtc tgttattgcc aagcacttaa 480
agggggagaat tggaaaacaa tgtagggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt attta ccaggcacac aagagactgg 600
ggaacagatg ggcagaaatc gcaaagctac tgcctggacg aactgataat gctatcaaga 660
accactggaa ttctacaatg cgtcggaagg tcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttccagaa gaacagtcac ttgatgggtt 780
ttgctcaggc tccgcctaca gctcaactcc ctgccactgg ccagccact gttaacaacg 840
actattccta ttaccacatt tctgaagcac aaaatgtctc cagtcattgt ccataacctg 900
tagcgttaca tgtaaatata gtcaatgtcc ctccagcagc tgccgcagcc attcagagac 960
actataatga tgaagaccct gagaaggaaa agcgaataaa ggaattagaa ttgct cctaa 1020
tgtcaaccga gaatgagcta aaaggacagc aggtgctacc aacacagaa caccatgca 1080
gctaccccggtgtggcacagc accaccattg ccgaccacac cagacctcat ggagacagt 1140
cacctgtttc ctgtttggga gaacaccact ccactccatc tctgccagcg gatcctggct 1200
ccctacctga agaaagcgcc tcgccagcaa ggtgcatgat cgtccaccag ggcaccattc 1260
tggtataatgt taagaacctc ttagaatttg cagaaacact ccaatttata gattctttct 1320
taaacacttc cagtaaccat gaaaactcag acttggaaat gccttcttta acttccaccc 1380
ccctcatttg tcacaaattg actgttacaa caccatttca tagagaccag actgtgaaaa 1440
ctcaaaagga aaatactgtt tttagaaccc cagctatcaa aaggtcaatc ttagaaagct 1500
ctccaagaac tcctacacca ttcaaacatg cacttgcagc tcaagaaatt aaatacggtc 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620

```

228/292

```

aacaggaatc tgatgaatct ggatttgttg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt caccgagacc tcgcctgtgc 1800
gagatgcacc gaatattctt acaagctcog ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaacaggtc cctggcgagc cccttgcagc 1920
cttgtagcag tacctgggaa cctgcatcct gtggaagat ggaggagcag atgacatctt 1980
ccagtcaagc tcgtaaatac gtgaatgcat tctcagcccg gacgctggtc atgtgagaca 2040
tttccagaaa agcattatgg ttttcagaac agttcaagtt gacttgggat atatcat tcc 2100
tcaacatgaa acttttcatg aatgggagaa gaacctatit ttgttgttgt acaacagttg 2160
agagcacgac caagtgcatt tagttgaatg aagtcttctt ggatttcacc caactaaaag 2220
gattttttaa aataaataac agtcttacct aaattattag gtaatgaatt gtagccagtt 2280
gttaatatct taatgcagat ttttttaaaa aaaaacataa aatgatttat ctggtatttt 2340
aaaggatcca acagatcagt attttttctt gtgatgggtt ttttgaaatt tgacacatta 2400
aaaggtactc cagtatttca cttttctcga tcaactaaaca tatgcatata tttttaaaaa 2460
tcagtaaaag cactactcta agtgtagact taataccatg tgacatttaa tccagattgt 2520
aaatgctcat ttatggttaa tgacattgaa ggtacattta ttgtaccaaa ccattttatg 2580
agttttctgt tagcttgctt taaaaattat tactgtaaga aatagtttta taaaaaatta 2640
tatttttatt cagtaattta attttgtaaa tgccaaatga aaaacgtttt ttgctgctat 2700
ggtcttagcc tgtagacatg ctgctagtat cagaggggca gtaga gcttg gacagaaaga 2760
aaagaaactt ggtgttaggt aattgactat gcactagtat ttcagacttt ttaattttat 2820
atataatatac attttttttc cttctgcaat acatttgaaa acttgtttgg gagactctgc 2880
attttttatt gtggtttttt tgttattgtt ggtttataca agcatgcgtt gcacttcttt 2940
tttgggagat gtgtgttgtt catgttctat gttttgtttt gtgtgtagcc tgactgtttt 3000
ataatttggg agttctcgat ttgatccgca tccctgtgtg tttctaagtg tatggtctca 3060
gaactgttgc atggatcctg tgtttgcaac tggggagaca gaaactgtgg ttgatagcca 3120
gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaacttttg agatatgac g 3180
gtgtacttac tgccttgtag caaaataaag atgtgccctt atttt 3225

```

<210> 356

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9
(a cellular retroviral nucleic acid binding
protein) (ZNF9) gene.

<400> 356

```

gtagttaaat gcagaaagtc ggtttttttc caccctttc ctctttttac acggcaagta 60
aagctcactg gcctgggagt tgcctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaataa tacaaccatc aatcagaaaa aggaggggag acaaaggaaa ataattagtc 180
tgtagctcaa ttgtgcattc ccgtgcaagg tgccctgact cgccacagcg gtaacagttg 240
acttcacttg tcttgctgca gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgcagtcttt tttgaatgtg tcccgaaatc tcccacaaga atancctttc 360
tgctcanct 369

```

<210> 357

<211> 1500

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1500)
 <223> zinc finger protein 9 (a cellular retroviral
 nucleic acid binding protein) (ZNF9) gene.

<400> 357
 gaattccaaa cagcctctac cttgcgagcc gtcttcccca ggcttgcgtc cgagtctccg 60
 ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120
 ttcaagtgtg gacgatctgg ccactggggc cgggaatgtc ctactgggtg aggcctgggt 180
 cgtggaatga gaagccgtgg cagagggtgt tttacctcgg atagagggtt ccagtttgtt 240
 tctctgtctc ttccagatat ttgttatcgc tgtggtgagt ctggtcatct tgccaaggat 300
 tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360
 tgcaaggagc ccaagagaga gcgagagcaa tgcgtctaca actgtggcaa accaggccat 420
 ctggctcgtg actgcgacca tgcagatgag cagaaatgct attcttgttg agaattcgga 480
 cacattcaaa aagactgcac caaagtgaag tgctataggt gtggtgaaac tggatcatgta 540
 gccatcaact gcagcaagac a agtgaagtc aactgtttacc gctgtggcga gtcagggcac 600
 cttgcacggg aatgcacaat tgaggctaca gcctaattat tttcctttgt cgcccctcct 660
 ttttctgatt gatggttgta ttattttctc tgaatcctct tcaactggca aagggttgga 720
 gatagaggca actcccaggc cagtgcgtt tacttgccgt gtaaaaggag gaaaggggtg 780
 gaaaaaaacc gactttctgc atttaactac aaaaaagtt tatgtttagt ttggtagagg 840
 tgttatgtat aatgctttgt taaagaacct ctttccgtg ccactggtga atagggattg 900
 atgaatggga agagttgagt cagaccagta agccgtcct gggttccttg aacatgttcc 960
 catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020
 ttagtataat gatggctctg gattgtctga cctcagtagc tattaataaa catcaagtaa 1080
 catctgtatc aggccctaca tagaacatac agttgagtgg gagtaaaca aaagataaac 1140
 atgcgtgtta atggctgttc gagagaaatc ggaataaaag cctaaacagg aacaacttca 1200
 tcacagtgtt gatgtt ggac acatagatgg tgatggcaaa ggtttagaac acattatttt 1260
 caaagactaa atctaaaacc cagagtaaac atcaatgctc agagtttagc taattttggag 1320
 ctattcagga attgcagaga aatgcatttt cacagaaatc aagatgttat ttttgtatac 1380
 tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaaag tcaga tggaa 1440
 agagcaactg aagtctaga aaatagaaat gtaattttaa actattccaa taaagctgga 1500

<210> 358
 <211> 425
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(425)
 <223> 3' terminal sequence. camp responsive
 element modulator (CREM) gene.

<400> 358
 ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaatgt 60
 tcagatatatt aaatgagcac caaacactac aaagtgcac caacatggtt ctattaaaaa 120
 ctncntttga ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180
 actaatataa aaatctgcaa atgccatata ttcatatcta ggctatttct cncatatagg 240
 catgtcatta gatagacttt ctttctattc tttccngagg natttttttg nggtttacnt 300
 ttattgnact gctggatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360
 gcaataaatt ttattg cata ggacacnatt ggtgncacat agaatgggag cngcaagtat 420
 gtggc 425

<210> 359

230/292

<211> 232
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(232)
 <223> 5' terminal sequence. camp responsive
 element modulator (CREM) gene.

<400> 359
 ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60
 agcttttctt gtttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120
 gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagttgtctg gccagcttag 180
 tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360
 <211> 1431
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:prime r

<220>
 <221> misc_feature
 <222> (1)..(1431)
 <223> camp responsive element modulator (CREM)
 gene.

<400> 360
 atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60
 agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120
 tgcagtgagc tgagatcagg caccagaaga ggctccccag ctgtaactct agtgcagtta 180
 ccttcgggcc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240
 cagtcatcag aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300
 gaatcagaag gtgtaattga ttctcataaa cgtagagaaa t cctttcacg aagaccctct 360
 tataggaaaa tactgaatga actgtcctct gatgtgctg gtgttcccaa gattgaagaa 420
 gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480
 atatatcaga ctagcacggg gcaatacatt gctatagccc aaggtggaac aatccagatt 540
 tctaaccag gatctgatgg tgttcaggga ctgcaggcat taacaatgac aaattcagga 600
 gctcctccac caggtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660
 cagttccttg tcccaggcag ccaggttgtt gttcaagctg ccactggtga catgccaaact 720
 taccagatcc gagctcctac tgetgctttg ccacaggagg tggatgatggc tgcacgccc 780
 ggaagtttgc acagtcccc aagcagctggca gaagaagcaa cacgcaaacg agagctgagg 840
 ctaatgaaaa acagagaagc tgcccgggag tgtcgcagga agaagaaaga atatgtcaaa 900
 tgtcttgaaa atcgtgtggc tgtgcttgaa aacaaaaca agactctcat tgaggaaactc 960
 aaggccctca aagatcttta ttgccataaa gtagagtaac tgtctttgac ttggaccttg 1020
 ttactctaa tcaaggcagg agatgcagca gtccacttta ttgccatgtg gacttgtggg 1080
 aaggacacgt gtgaccctta agaatccagt ttggattagt gtttgaaatt gaattgggaa 1140
 tgttggtcca ggatgtggaa tgcagcgtga tcacacttac cgagcttact ttgatctgtt 1200
 tgtcaatagc atgc aaaaaa tgctttgttt gccctttgct tctgcttttt ttcaggggaa 1260
 ctgccaaaga atgtcgacgt cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320
 cagtgtgga agtccagaac aagaagctta tagaggaact tgaaaccttg aaagacattt 1380
 gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

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<210> 361
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 3' terminal sequence. cathepsin b (CTSB)
gene.

<400> 361
caagttggag aaacctttta ttggcacagg cattccttgt taacttgaca ggggtgaagct 60
gtaatttttc aaaaacagta aaagctgggt tctcctaaac tattttcctt gtggtagtag 120
agatcagtgg gtcagaaaca actcctgacc acttggtttc cttttgagcc gcgtcattag 180
gaggcaatct gtaaaactag cacagggtct ccgctgttcc actggctcac ccacatg att 240
agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300
gaggtttgta cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360
agggtcccca acaccatctc tctctgatt tctgtgacaa atgtggaagc tacttgcttg 420
gagggtactgg gggaactgat gggggaactt tcatc cg 457

<210> 362
<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60
tcacatgatt agtactgcta ggggacctac taaaatttta acactgactt attattagag 120
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaaattc 180
aagcaaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgct g gcncttaagg 240
tgaataagggt ggtgggtgact gttctgcaga gagttttctca taagcagggt gagcattggg 300
aaccacagggt tcacagtttt tctcttgaag agacactttg ctgtcccgat gatcaaacc 360
ttcttgtggg catcttctg ttaaggcaca ttgaggccaa c 401

<210> 363
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. melan -a (MLANA) gene.

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<400> 363

```

attaaggaag gtgtcctgtg ccctgacctt acaagatgcc aagagaagat gctcacttca 6 0
tctatgggta ccccaagaag gggcacggcc actcttacac cacggctgaa gaggccgctg 120
ggatcggcat cctgacagtg atcctgggag tcttactgct catcggtgtg tgggtattgt 180
gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240
cttaacaaga agatgcccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300
agagaaaaac tgtgaacctg tggttcccaa tgctccacct gcttatggag aaactctctg 360
cagaacagtc

```

<210> 364

<211> 1524

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1524)

<223> melan-a (MLANA) gene.

<400> 364

```

agcagacaga ggactctcat taaggaagggt gtccgtgtgcc ctgaccctac aagatgccaa 60
gagaagatgc tcacttcatac tatgggttacc ccaagaagggt gcacggccac tcttacacca 120
cggctgaaga ggccgctggg atcggcatcc tgacagtgat cctgggagtc ttactgctca 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggttt gatcatcggg 300
acagcaaagt gtctcttcaa gagaaaaact gtgaacctgt gggtccc aat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttacacctta gagccagcga 420
gacacctgag acatgctgaa attattttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtc tccttttgaa tgggtgtagg aaaaatgcaag ccactctctaa taataagtca 540
gtgttaaaat tttagtaggt ccgct agcag tactaatcat gtgaggaaat gatgagaaat 600
attaaattgg gaaaactcca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660
gtaatgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt ggggtattctg 720
gggccatcca atttctcttt acttgaaatt tggctaataa caaactagtc aggttttcga 780
accttgaccg acatgaactg tacacagaat tgttccagta ctatggagtg ctcaaaagg 840
atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900
agcaatgtct ctttgtgtct taaaattcta ttatactaca ataataatatt gtaaagatcc 960
tatagctctt tttttttgag atggagtctt gcttttgttg ccag gctgg agtgcaatgg 1020
cgcgatcttg gctcaccata acctccgctt ccagggttca agcaattctc ctgccttagc 1080
ctcctgagta gctgggatta caggcgtgag ccactatgcc tgactaattt tgtagtttta 1140
gtagagacgg ggtttctcca tgttgggtcag gctgggtctc aactcctgac ctgaggtgat 1200
ctgcccgcct cagcctccca aagtgtctgga attacaggcg tgagccacca cgctgggctg 1260
gatcctatat cttaggtgaa acatataacg cagtctaatt acatttcact tcaaggctca 1320
atgctattct aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
aataagtaaa agctactatg tactgcctta gtgctgatgc ctgtgtactg ccttaaatg t 1440
acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
aatcataaag gatcagagat tctg

```

<210> 365

<211> 556

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

233/292

<221> misc_feature
<222> (1)..(556)
<223> 3' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 365
actattcggtt aggcgttttat ttttctctat gttctgcagt aactaaggaa aatcatggta 60
aatgtcaatc ttcacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120
atcctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgtagc 240
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttccatta 360
tcaaaaaagca aacactctat ttgcgagttg aacaatgatc actgatcaca aatatacnaat 420
acagtgtccc ccgcccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480
ctgggggtac ccgtgactcc nccttttacac cccccagggg ctggcctcag atctacctaa 540
ggggnnggat aacccc 556

<210> 366
<211> 464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(464)
<223> 5' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 366
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga 60
cgtcagcaca gcattcttgg agatccgaag aagatcgtca cagaagagtt tgtgcgcaga 120
gggtacctga tttataaacc ggtgccccgt agcagtcagg tggagtatga gttcttctgg 180
gggccccgag cacacgtgga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcgga cgatgatgca 300
gagggtgagg ctatcctcaa ttcaggtgct aggggttatt ccgcccccta agtagatctg 360
gaggcagacc cttgggggtt gtaaaagaga gtnacaggta ccccaaaagg agtagatg nc 420
aaggggccct aagttgcaaa atgatgtcga ttttggggcc gggg 464

<210> 367
<211> 1476
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1476)
<223> apr-1 protein (APR-1) gene.

<400> 367
ctggaagaat tcgctgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcgggct 60
tgcagctgcg gcaagtgtcg gcggcggctg ctgcgcgaag tcagctggcg tgggaactac 120
cctttgtagc tgagaacggc ttgtttattg ctacaaagac tctattgaca ttggtagctt 180
cagcggcagc agcttcttac ggtataaagc tgttgcttcc tgaagaggct acaagcatcc 240

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ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtcggcgcc gccgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gcctctgttg tagcgagcac ccccgaaga c 420
gacctgagcg gccccgagga agacccgagc actccagagg aggcctctac caccocctgaa 480
gaagcctcga gcaactgcca agcacaaaag ctttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcatcatggg caacagcgcc 600
aaggaagctc tggctctggaa agtgctgggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatctttg gagatccgaa gaagatcgtc acagaagagt ttgtgcgcag aggggtacctg 720
atttataaac cgggtgccccg tagcagtcctg gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actggccttg taattatgac tgggattcgg acgatgatgc agagggttag 900
gctatcctca attcaggtgc taggggttat tccgcccctt aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtac cccaaggagt agatgccagg gtcctaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtgat cagtga tcat 1080
tgttcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttcogtttgt tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgttca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaa aatgttgaa aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgtatc tctttttatt ttcggattgc ttatca 1476

```

<210> 368

<211> 436

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(436)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 368

```

cgtttttttg ctttaaatac caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat caggggcaaaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaaaa taaaagtcac ccacactcag ccacgtgatt gggaagagaa 180
agggggcttg ctcctacttg cgaccacatg gccgggtggg tcccaa gagt agccatgggt 240
tatgattttg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggtaa tatttcagat tcagctagaa gagctttcca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct ccccaactta gcctacttac ttttcnaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436

```

<210> 369

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

235/292

<400> 369
ggttgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
ccgctctctc cgctattact atgaaaaggg catcatgcag aagggtggctg gagagcgata 120
cgtctacaaa tttgtctgtg acccagatgc cctcttctcc atggctttcc cggataacca 180
gcgtccgttc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca cctgcccgt 240
gaccacattt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300
ctatgccgaa ggtttgctta ctaagtttct gagtggcgga gtgnccaaac cctaggagct 360
agcagttccc attcagggca aacaagnngc agtgnggttt gtt ttgtgtt tttt 414

<210> 370
<211> 249
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(249)
<223> 5' terminal sequence. cd69 antigen (p60,
early t-cell activation antigen) (CD69) gene.

<400> 370
ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
cccngacgc 249

<210> 371
<211> 1702
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1702)
<223> cd69 antigen (p60, early t-cell activation
antigen) (CD69) gene.

<400> 371
agactcaaca agagctccag caaagacttt cactgtagct tgacttgacc tgagattaac 60
tagggaatct tgagaataaa gatgagctct gaaaattggt tcgtagcaga gaacagct ct 120
ttgcatccgg agagtggaca agaaaatgat gccaccagtc ccattttctc aacacgtcat 180
gaagggtcct tccaagttcc tgtctgtgtg gctgtaatga atgtggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaataca attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccattgtttc tcatgc tctg aggactgggt tggctaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgcat gtagagagga aactggggtt ggactgaaaa aggaacctgg tcacccatgg 540
aagtgggtcaa atgg caaaga atttaacaac tgggtcaacg ttacagggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc cataga gact 780

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ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacaggttga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggtg ctagatactg aatgtaaaca aaggaattat ggctggtaac ataggttttt 1140
agtctaattg aatcccttaa actcagggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatcttct tctttttaga gaaatttgcc aattttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtattta tttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacataattt ctttgccctt ataatctttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aa                                     1702

```

<210> 372

<211> 585

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(585)

<223> 3' terminal sequence. oncogene tc21 (TC21) gene.

<400> 372

```

gtaggcagta tgattccaaa agttaaaaat tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaat gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat atttttaa aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcttt tcctggccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcngg tgaaggagga cattcctggc cctggaaatt tccnggataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc cggatgccnc catgtatgtt 540
acctaagctg ccggcaacg tngcctctnc cggggtagcc gcc ng 585

```

<210> 373

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. oncogene tc21 (TC21) gene.

<400> 373

```

gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

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acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gagttcccaa tgattt taat tggtaataaaa 240
gcagatctgg atcatcaaag acaggtaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcatcagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttattc aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaaagaa aagccagaaa gctg cattgt g 451

```

<210> 374

<211> 425

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 374

```

gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atattttcaa 120
aacacagata aatagttttac tacagataaa tagcttcacc c tttggtgtc ctcccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaaagcaat gcccagggat taggctatgg aagggcaaaa tggaccatt 300
caaatttcct cccagggacc aggccttatt aaccctggga aatgtcctta gctgggtggg 360
gaaaggttgg cgattcagga atacatatgt gtagtttttg ttagaagcca tccatagcac 420
acccg 425

```

<210> 375

<211> 478

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 375

```

ggcgtttccag ttcccacttg gaggccnttc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttcttgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctggg aggaaatttg aatgggtcca ttttgccctt 180
ccatagccta atccctgggc attgctttcc actgaggttg ggggttgggg tgtactagt 240
acacatcttc aacagacccc ctctangaaa tttttcagat gcttctggga gacacccaaa 300
ggggaaagct attta tctgt agtaaaactat ttatctgtgt ttttgaaata ttaaaccctg 360
gatcagtcct ttgatcagta taaatttttt aaagttactt ttgtcagagg caccaaaggg 420
tttaaactga ttcataaata aatatcngga cttcctcgat cttccaaaaa aaaaaaaa 478

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<210> 376
 <211> 1794
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1794)
 <223> cd44 antigen (homing function and indian
 blood group system) (CD44) gene.

<400> 376
 cccgcgccct ccgttcgctc cggacacccat ggacaagttt tggtaggcacg ca gcctgggg 60
 actctgcctc gtgccgctga gcctggcgca gatcgatttg aatataacct gccgctttgc 120
 aggtgtattc cacgtggaga aaaatggtcg ctacagcatc tctcggacgg aggccgctga 180
 cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240
 catcgatttg gagacctgca ggtatgggtt c atagaaggg catgtggtga ttccccggat 300
 ccaccccaac tccatctgtg cagcaaaca cagaggggtg tacatcctca catacaaac 360
 ctcccagtat gacacatatt gcttcaatgc ttcagctcca cctgaagaag attgtacatc 420
 agtcacagac ctgcccgaatg cctttgatgg accaattacc ataactattg ttaaccgtga 480
 tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540
 caaccctact gatgatgacg tgagcagcgg ctccctccagt gaaaggagca gcacttcagg 600
 aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660
 gatcacggac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720
 tgggggggtcc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780
 aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840
 catcttggca tccctcttgg ccttggcttt gattcttgca gtttgcattg cagtcaacag 900
 tcgaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960
 ggacagaaag ccaagtggac tcaacggaga ggccagcaag tctcaggaaa tggatgcat 1020
 ggtgaacaag gactcgctcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080
 cctgcagaat gtggacatga agattggggg gtaacaccta caccattatc ttggaaagaa 1140
 acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200
 actgattgtt tcattgcgaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260
 tgttttgttc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320
 cccaattaat aatcagcaag aatttgatcg ttcagttcca cttg gaggcc ttcacccctg 1380
 ggtgtgctat ggatggcttc taacaaaaaac tacacatatg tattcctgat cgccaacctt 1440
 tccccacca gctaaggaca tttcccaggg ttaatatggc ctggtccctg ggaggaaatt 1500
 tgaatgggtc cattttgccc ttccatagcc taatccctgg gcattgcttt ccactgaggt 1560
 tgggggtgtac tagttacac tcttcaacag accccctcta gaaatttttc agatgcttct 1620
 gggagacacc aaagggtgaa gctatttatc tgtagtaaac tatttatctg tgtttttgaa 1680
 atattaaacc ctggatcagt cctttgatca gtataatttt ttaaagttac tttgtcagag 1740
 gcacaaaagg gtttaaaactg attcataata aatatctgta cttcttcgat cttc 1794

<210> 377
 <211> 452
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(452)
 <223> 3' terminal sequence. cyclin -dependent
 kinase inhibitor 3 (cdk2 -associated dual
 specificity phosphatase) (CDKN3) gene.

```

<400> 377
ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctgggtggttt catttcaata caaattatgc tagagaactg acatttcaga catggtcata 120
tatatgctat ttgaattcct ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgt cccgaaactc atgaagataa ttgtattgct tgatggctctg 240
tattgccccg gatcctctta ggtctcgcag gctgtctatg gcttgctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgtatt aagggttttc cggtaatttt t aaggcaggt tgtaagcnct tccattattt 420
cacagcagct ggccatgtcn ggagtcccc ca 452

```

```

<210> 378
<211> 472
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(472)
<223> 5' terminal sequence. cyclin -dependent
        kinase inhibitor 3 (cdk2 -associated dual
        specificity phosphatase) (CDKN3) gene.

```

```

<400> 378
ggcacgagcg gcaactggtc tcgacgtggg gcggccanga ctgaagccca ngtnntcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg tttatgtgct 180
cttccagggt gttaaatttaa agatgttaga agaaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatttgt tttctgcacc agaggggaac tgtcaaaaata 300
tagagtccca aaccttctgg atctctacca gcaatgtgga attatcacc atcatcatcc 360
aatccgcaga tggaggggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472

```

```

<210> 379
<211> 639
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(639)
<223> cyclin-dependent kinase inhibitor 3
        (cdk2-associated dual specificity phosphatase)
        (CDKN3) gene.

```

```

<400> 379
atggagccgc ccagttcaat acaaacaagt gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttccagg tgtaaattta aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatttgt tttctgcacc 240
agaggggaac tgtcaaaaata tagagtccca aaccttctgg atctctacca gcaatgtgga 300
attatcacc atcatcatcc aatcgcatg ggagggactc ctgacatagc cagctgctgt 360
gaaataatgg aagagccttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420

```

240/292

```
tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tectactata cctgtctgac 480
acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540
cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600
tcatcaagag attcacaatc aagatctgta tcaagataa 639
```

<210> 380

<211> 487

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(487)

<223> 5' terminal sequence. max-interacting
protein 1 (MXI1) gene.

<400> 380

```
aagtggcgac tggaacagct gcagggtcct caggagatgg aacgaatacg aatggacaga 60
attggatcaa ctatttcttc agatcgttct gattcagagc gagaggagat tgaagtggat 120
gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180
gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgcc 240
gtgtcaaact ttcatctact tcatagaacc cagcatgaca taacagtgcg gggaaaatat 300
tactgtggcc attcatacaa acaatctctt aaattgggtt catgatgcag tctcctcttt 360
aaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420
caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480
catttta 487
```

<210> 381

<211> 2416

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2416)

<223> max-interacting protein 1 (MXI1) gene.

<400> 381

```
agattatgat cgcttgaggc ccctctccta cccagatacc gatgttatac tgatgtgttt 60
ttcctttttt tttttttttt ttttaagtaat taagggtagt taaattatth aaagtataca 120
aagtccaaac agccaggggt aaggtctcca agaggccttc ccagggttag ggagtgcgga 180
gaggccccgg tcgccaccgg cgggtgccat ggagcgggtg aagatgatca acgtgcagcg 240
tctgctggag gctgccgagt ttttggagcg ccgggagcga gagtgtgaac atggctacgc 300
ctcttcattc ccgtccatgc cgagcccccg actgcagcat tcaaagcccc cagcgagggt 360
gagccgggca cagaaacaca gcagcgggac gagcaacacc a gcaactgcca acagatctac 420
acacaatgag ctggaaaaga atcgacgagc tcatctgcgc ctttgtttag aacgcttaaa 480
agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540
agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600
gaattttgaa cgagaacaga gattttttaa gtggcgactg gaacagctgc agggtcctca 660
ggagatggaa cgaatacgaa tggacagcat tggatcaact atttcttcag atcgttctga 720
ttcagagcga gaggagattg aagtggatgt tgaaagcaca gaggttctcc atggagaagt 780
ggacaatata agtaccacca gcatcagtga cattgatgac cacagcagcc tgccgagtat 8 40
tgggagtgac gagggttact ccagtgcagc tgtcaaactt tcattcactt catagaacct 900
```

241/292

```

agcatgacat aacagtgcag ggcaaaatat tcactggggcc aattcaatac aaacaatctc 960
ttaaattggg ttcattgatgc agtctcctct ttaaaacaaa acaaaacaaa acaaaactat 1020
acttgaacaa aagggtcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttggtgtg aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctcgttt gctcatacta cattgagtag acacatttaa 1260
ggatgggggt atg aaccctt cctgagcttt atggtcctaa aagcaaaata aaaactattc 1320
gaatgaaaag acaagaaaat caggtattaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgac aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcattgctc gcaaaaggag agactcccat ga agcctttt 1500
gaaagggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaacctt 1560
atcctgcatt gtttagcata ggcaccacgc tgccacctct ccattcctgct gcccttaggc 1620
cacatgggag cagtccatgc atgacagcct ctatcctaca aggcctatga gtatggattg 1680
ggggggccaa aaggaaaaag ctccatg tgc ctctttgtct gcgtgggtca gaagagttgt 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aaccaaatac acatcttttt aaagcttatc cataaaaaaa 1860
aatagatgtc ttttatatgt gaaaaacaca tggggaaaaa aatcatctat tttgatgcag 1920
catttgataa tgataaaaaa cctcacacct cactctttat agtgcacaaa atgaatgagg 1980
tctgggctag gtagaaaaag ggtcaatgct atttttgttt ttagaatcat taccttttac 2040
cagcttttaa ccattctgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcacttgt ctcattttaa tgtaaagatt tgcttccatt ttcctacagg cagtctctct 2160
cttcctcaca gtcccactgt gcaggtgcta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaag tttctagcct gcactttgat gtcatgtgtt ccctttgtct 2280
ttcaaactcc aaggttcccc tgtggccctc tcccttacct tgggaaggcc tcttgagac 2340
cttaccctg gctgt ttgga ctttgtatac ttaataaat ttaactacct ttaattactt 2400
aaaaaaaaa aaaaaa 2416

```

<210> 382

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. homeo box a5 (HOXA5)
gene.

<400> 382

```

tttttttttt ttgttatagt tacttcaagt aacacagctt gcttcatata aataagttaa 60
aacatctatt ttttttcaag acaaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgc tata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggatc cgctaaatac tgctcagtag tttaaacgct cagatactca 300
gggacggaag gccctccctt gcccgcggn c atnctccatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc 378

```

<210> 383

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

242/292

<221> misc_feature
<222> (1)..(439)
<223> 5' terminal sequence. homeo box a5 (HOXA5)
gene.

<400> 383
aaatcaagca cacatanttan aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60
cgctatccaa atggcccgga ctaccagttg cataattatg gagatcatag ttccgtganc 120
gagcaattca gggactcggc gagcatgcac tccggcaggt acggctacgg ctacaatggc 180
atggatctca gcgtcggcng ctcgngctcc ngcacttttg ctccggagag cgcgcccga 240
gctacgtnc aagccacgc ggcncactcc aagcccaggt acagcnagcc ggccacgtcc 300
acgcactctn cctcancncg atccgctgcn ctgctccgnc gtngggccct tcgcccngga 360
ancgacanna ccaanggcgg gaaaaactcc cttaaggca a ctccagcngg cgcctcgggc 420
cgacngccgg aagcaccca 439

<210> 384
<211> 813
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(813)
<223> homeo box a5 (HOXA5) gene.

<400> 384
atgagctctt attttgtaaa ctcatcttgc ggctcgtatc caaatggccc ggactaccag 60
ttgcataatt atggagatca cagttccgtg agcagagcaat tcagggactc ggcgagcatg 120
cactccggca ggtacggcta cggctacaat ggcattggatc tcagcgtcgg ccgctcgggc 180
tccggccact ttggctccgg agagcgcgcc cgcagctacg ctgccagcgc cagcgcggcg 240
cccggcgagc ccaggtacag ccagccggcc acgtccacgc actctcctca gcccgatccg 300
ctgccctgct ccgccgtggc cccctcgccc ggcagcgaca cgcaccacgg cgggaaaaac 360
tccttaagca actccagcgg cgctcgggcc gacgcgggca gc acccacat cagcagcaga 420
gaggggggtg gcacggcgtc cggagccgag gaggacgccc ctgccagcag cgagcaggcg 480
agtgcgcaga gcgagccgag cccggcgccg cccgcccac cccagatcta cccctggatg 540
cgcaagctgc acataagtca tgacaacata ggcgggcccg aaggcaaaaag ggcccggagc 600
gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660
accgcagaa ggaggattga aatagcacat gctctttgcc tctccgagag acaaattaaa 720
atctggttcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780
atggccgcgg caggaggggc cttccgtccc tga 81 3

<210> 385
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(447)
<223> 3' terminal sequence. x-box binding protein
1 (XBP1) gene.

<400> 385

243/292

```

gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca cttttcagaa 60
gctacactag caggaaaaaa ttccatcaag catttacata gtaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcagggtgtt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaattgac cttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttontacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc                                     447

```

<210> 386

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 5' terminal sequence. x-box binding protein

1 (XBP1) gene.

<400> 386

```

aagaacctgt agaagatgac ctcggtccgg agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tcctgcctac tggatgctta cagtgactgt ggatacgggg 120
gttccctttc cccattcagt gacatgtcct ctctgcttgg tgtaaaccat tcttgggagg 180
acacttttgc caatgaactc tttcccca gc tgattagtgt ctaaggaatg atccaatact 240
gttgcccttt tccttgacta ttacactgcc tggaggatag cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaga 360
tctcatagat gacccccagg tattgtcttt tgacatccca agcagtccea ggtattggag 420
acataattact ggaagtaaaa gaaatattac tnataattgg ag                                     462

```

<210> 387

<211> 1836

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1836)

<223> x-box binding protein 1 (XBP1) gene.

<400> 387

```

ggcgctgggc ggctgcggcg cgcggtgcgc ggtgcgtagt ctggagctat ggtggtggtg 60
gcagccgcgc cgaaccgcgc cgacgggacc cctaaagttc tgcttctgtc ggggcagccc 120
gcctccgcgc cggagccccc ggccggccag gccctgccgc tcatgggtgcc agcccagaga 180
ggggccagcc cggaggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgcctc 240
acgcacctga gccccgagga gaaggcgctg aggaggaaac tgaaaaacag agtagcagct 300
cagactgcc a gagatcgaaa gaaggctoga atgagtgagc tggaacagca agtggttagat 360
ttagaagaag agaaccaaaa acttttgcta gaaaatcagc ttttacgaga gaaaactcat 42 0
ggcctttagt ttgagaacca ggagttaaga cagcgcttgg ggatggatgc cctggttgct 480
gaagaggagg cggaagccaa ggggaatgaa gtgaggccag tggccgggtc tgctgagtcc 540
gcagcactca gactacgtgc acctctgcag cagggtgcag cccagttgtc acccctccag 600
aacatctccc catggattct ggcggtattg actcttcaga ttcagagtct gatatacctgt 660
tgggcattct ggacaacttg gaccagtc a tgctcttcaa atgcccttc ccagagcctg 720

```

244/292

```

ccagcctgga ggagctccca gaggtctacc cagaaggacc cagttcctta ccagcctccc 780
tttctctgtc agtggggacg tcatcagcca agctggaagc cattaatgaa ctaattcgtt 840
ttgaccacat atataccaa g cccctagttc tagagatacc ctctgagaca gagagccaag 900
ctaattgtgt agtgaaaatc gaggaagcac ctctcagccc ctcagagaat gatcacccctg 960
aattcattgt ctcaagtgaag gaagaacctg tagaagatga cctcgttccg gagctgggta 1020
tctcaaactc gctttcatcc agccactgcc caaagccatc ttccctgccta ctggatgctt 1080
acagtactg tggatacggg gggtcccttt ccccatcag tgacatgtcc tctctgcttg 1140
gtgtaaacca ttcttgggag gacacttttg ccaatgaact ctttcccag ctgattagt 1200
tctaaggaat gatccaatac tgttgccctt ttcccttgact attacactgc ctggaggata 1260
gcagagaagc ctgtctgtac ttcatcctaa aagc caaaat agagagtata cagtcctaga 1320
gaattcctct atttgttcag atctcataga tgacccccag gtattgtctt ttgacatcca 1380
gcagtcctaa gtattgagac atattactgg aagtaagaaa tattactata attgagaact 1440
acagctttta agattgtact tttatcttaa aagggtggta gttttcccta aaatacttat 1500
tatgtaaggg tcattagaca aatgtcttga agtagacatg gaatttatga atgggtcttt 1560
atcatttctc ttcccccttt ttggcatcct ggcttgctc cagttttagg tcctttagtt 1620
tgcttctgta agcaacggga acacctgctg agggggctct ttccctcatg tataactcaa 1680
gtaagatcaa gaatcttttg tgaaattata gaaatttact atgtaaat gc ttgatggaat 1740
tttttctgc tagtgtagct tctgaaagg gctttctcca tttattttaa actacccatg 1800
caattaaaag gtacaatgca aaaaaaaaaa aaaaaa 1836

```

<210> 388

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 388

```

tttttcttaa ataatttatt ttttaatggt gactcttggt aaaagttaca tttattttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggctttcta ttagggacaa ttaaagtgtgc 120
aaatttcaaa tactttttat aataagtata aataattact ttttttcaca ttaagaatgg 180
aaataatgat caacacaana tattaagata tcaactttta gagaattaga tgaaaacact 240
gaagtttatt tgngtatcct tggaangaa ttataaagat tcgtctggga aaaactt agg 300
gggctctaag gggaaagttg tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggcctt aagtacagac ccccnaaatg gcagccttta tcnccgggga 420
aatgcattt ccc 433

```

<210> 389

<211> 206

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 389

245/292

```

ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc actttattta 60
ttttattaca aacttcaaga ttatttaagt gaagatatatt cttcagctct ggggaaaatg 120
ccacagtgtt ctcctgagag aacatccttg ctttgagtca ggctgtgggc aagttcctga 180
ccacagggag taaattnngn cctctt 206

```

<210> 390

<211> 4426

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein
3 (TNFAIP3) gene.

<400> 390

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gcctcctgca agaacatctt ggctgcccgc agcgaggagc tctgcatgga gtgtcagcat 2280
cccaaccaga ggatgggccc tggggcccac cgggggtgagc ctgccccoga agaccccccc 2340
aagcagcggt gccgggcccc cgctgtgat cattttggca atgccaagtg caacggctac 2400

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tgcaacgaat gctttcagtt caagcagatg tatggctaac cggaacacagg tgggtcacct 2460
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<210> 391

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 3' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 391

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agtagaaacc actgacatac acactcacat tcaagcacac acactcactc aggcgcacac 180
acccacacac acatacccca gagccaccga ggaagggaaa caccaagggt cgctgcacat 240
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aacacacatt ataagcactt tgcoctgatc actcactngg gtctgtcttt tgtgggaagg 360
agaggaagaa ttcatacaaag gtctcctccc catgggtngg gggagtgggg agtgagtgag 420
tgatggtgga gtgaaacaag

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247/292

<210> 392
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(471)
<223> 5' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 392
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tgcagcaaag gggagccaga aatgggcagt tctcccaggg agtgagcagc tactgtaact 120
tttttaaatt aagacaaaaa gccttgaaga aaatgacttt atttttctaa gtgtaacctc 180
agtatttatg taattttgtac aggggccatg ccaaccccc cctccccct ttgngtnaga 240
ccttgagggt gggccagcat aggggggagg gtcttttacc ctgtgtcaga gcctaccttc 300
accacctata tccagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaatttt 360
cttaaccctt aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaaggg 420
atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393
<211> 4201
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4201)
<223> serum response factor (c-fos serum response
element-binding transcription factor) (SRF) gene.

<400> 393
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gcagacggac agggggcgct gcgcgcggcc tggggcaacc cgggccac ag gggcaggaaa 180
gtgaggggcc aggtcggccc gggcgtgcag gggccccggg ttgcagcgg cggccgcggc 240
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ggctgcggcg gctccgattc ctgcgtgact gcccgctcgc cctcctgcat cgagcgccat 360
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gccagactct ccacccggtt cag accccac aacagaccag agaatgagtg ccactggcctt 1080
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248/292

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aactgtgggt ggcacatga tgtaccctag cccgcatgcg gtgatgtatg cccccacctc 1620
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g 4201

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<210> 394

<211> 563

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<220>
 <221> misc_feature
 <222> (1)..(563)
 <223> 3' terminal sequence. sry (sex determining
 region y)-box 9 (campomelic dysplasia, autosomal
 sex-reversal) (SOX9) gene.

<400> 394
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 aaaagggaaa ggtaagtttc acggagagaa caaaagggtt ggggctggga gggaaacaag 120
 tgaacaaac aaaacacgaa cacaaaccaa agctttttacc taaagacaaa atatgattta 180
 aatgccaggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240
 attgaaggt gccatattat gagtgcctta agattttatt ctactgactt ctaaaactgt 300
 taatatatct ttttttaaat aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360
 aaactctcta gccacagcag taattaagat taaggctctgt cagtgggctg atccccctcca 420
 ggtagcctcc ctactccaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480
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<210> 395
 <211> 3936
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(3936)
 <223> sry (sex determining region y) -box 9
 (campomelic dysplasia, autosomal sex -reversal)
 (SOX9) gene.

<400> 395
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 ggcagctacg gcacgcagc caccgcggcc acccggcgga gcgcgggcca cgtgtggatg 1380
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atcaagacgg agcagctgag cccagccac tacagcgagc agcagcagca ctgcgcccaa 1620
cagatcgccct acagcccctt caacctccca cactacagcc cctcctaccc gcccatcacc 1680
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ttgtttacaa taaatataca tt gcattaaa aagaaa 3936

```

<210> 396

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(204)

<223> 3' terminal sequence. cadherin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 396

```

tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgaggttcac tggaggaggg caaagggtgg actagggagg 120

```

251/292

tgacccgcat gggccagatn ggagagaaac tcttcccacc ccggcagaag gggcctcttc 180
ctggccgccc catccanact cagg 204

<210> 397
<211> 458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(458)
<223> 5' terminal sequence. cadhe rin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 397
caggacgcct acgacatcag ccagctgcgt caccgcagag cgctgagcct gcctctggga 60
ccgcccgcac ttgcgagaga tgccccgcag ncagcctgca cccccagcca ccccgagtgc 120
tgcccaccag ccccttgga atcgccgact tcatcaatga tggcttgga g gctgcagata 180
gtgacccag tgtgccgcct tacgacacag cctcatcta tgactacgag ggtgacggct 240
cggtggcggg gacntgagct ccattcctgtc cagccagggc gatgaggacc aggactacga 300
ctacctcaga gactgggggc cccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360
cgggttngga gttacggggc cagatgg gac caccaggcca gggaggggtct ttctcctggg 420
gcactgctac ccagacacag aggcgggaca gcctgan 458

<210> 398
<211> 2833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2833)
<223> cadherin 15, m-cadherin (myotubule) (CDH15)
gene.

<400> 398
acttgcgctg tcaactcagcc tggacgcgct tcttcgggtc gggggtgcac tccggcccg 60
ctcccgccctc ggccccgatg gacgcgcgct tctcctcgt cctcgggctg ttggcccaga 120
gcctctgcct gtctttgggg gtt cctggat ggaggaggcc caccaccctg taccctggc 180
gcccggcgcc tgccctgagc cgcgtgcgga gggcctgggt catccccccg atcagcgtat 240
ccgagaacca caagcgtctc ccctaccccc tggttcagat caagtcggac aagcagcagc 300
tgggcagcgt catctacagc atccaggagc ccggcgtgga tgaggagccc cggggcgtct 360
tctctatcga caagttcaca gggaaggctt tctcaatgc catgctggac cgcgagaaga 420
ctgatcgctt caggctaaga gcgtttgccc tggacctggg aggatccacc ctggaggacc 480
ccacggacct ggagattgta gttgtggatc agaatgacaa ccggccagcc ttcctgcagg 540
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aggccacaga tgccgacgac cccgagacgg acaacgcagc gctgcgggtc tccatcctgc 660
agcagggcag ccccagctc ttcagcatcg acgagctcac aggagagatc cgcacagtgc 720
aagtggggct ggaccgcgag gtggctgcgg tgtacaatct gaccctgcag gtggcggaca 780
tgtctggaga cggcctcaca g ccaactgcct cagccatcat cacccttgat gacatcaatg 840
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900
gagtggatgt gggacgcctg gaagtggagg acagggacct gccaggctcc ccaaactggg 960
tggccagggt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

252/292

```

ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
actacgaact caaagtgtcg gtgcagaatg agggcccgct gcaggcggct gcccttaggg 1140
ctgagcgggg ccaggccaag gtccgcgtgc atgtgcagga caccaacgag ccccccgtgt 1200
tccaggagaa cccacttcgg accagcctag cagagggg gc acccccaggc actctggttg 1260
ccaccttctc tgcccgggac cctgacacag agcagctgca gaggetcagc tactccaagg 1320
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ccttcctgcc ggggtgggaa gagtttctct ccacggccc catgcgggtc acc tccctag 2760
tcccaccttt gcctcctacc agtgaacctc atctttgtat gaaagacagc aacctcctgg 2820
gtaaatctga atg 2833

```

<210> 399

<211> 646

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(646)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 399

```

tatctcacac tgtactttat ttttcttcac aatattaact agacagacaa ggaaagttta 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atgggtggcca 120
actggagact tactttacct taaccatgta aagtatcctt accgtatttt ttatgtgtac 180
agtgttgtag aatatcagcc acctcttaaa agtatcaatc ttaaaaaagag ccatggaagg 240
taaaagtatg aaaatcttga taacaaaagc tttcaataca aaaacactta ttgtacactt 300
atttttatatt aaaacaaaaa taac cccagt aactcaaaac aaaagcaaac cttgggttgaa 360
aacttaagaa ggtataataa acaaaaccac caaaagaaag cttcccaaaa agaaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaaaaa cttaatgaaa tgagctatct 480
ggagggccca cggagatttt ccaaaagggt taggtgcatg gatttactca gtatctacnt 540
acagtcttat ttattaatag ctacaganttc ctgattgagc gagcctttcc atctccacca 600
gtgtccccac ttctgtgcnc acttgggntg cagacaccct gtgttg 646

```

253/292

<210> 400
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 400
ggtattttaa caataaatgt gcagtttttaa ctaacaggat atttaatgac aaccttctgg 60
ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaaa aattttataa 1 20
aattaagcaa tgtgaaactg aattggagag tgataataca agtccttttag tcttaccag 180
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300
actgccccag aaaaataact tcaagcaaac atcctatcaa caacaagggtt gttctgcata 360
ccaagctgag cacagaagat gggaacaact gtggaggatg gaaaggctcg ctcaatcaag 420
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(419)
<223> 3' terminal sequence. ests (EST W73386)
gene.

<400> 401
gaaggtcatt cttgcgatgg gtttattgca ggagatgatg gaccaaattg ctctgacaca 60
tgcacacgct cctgggcacg cctgctgcgn gtncgcttcc catga cccc agggccctct 120
atgcctcccc cccagggcac cctgccact tgccccact tcatgtacca ccaagccctt 180
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagtg catgtggctc 240
agaacataaa agcatcttca acattcgtca ttgagccaaa cgaaacacag tgtttggctc 300
aagagccggc gacactngca tcc ctatcca cacgtggaac ctgcccttgg gcttngttga 360
ccggaggatn ggccgctctt ccttgtcatc cagcanccgg agcatgtatg tgcccaga 419

<210> 402
<211> 568
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(568)
<223> 3' terminal sequence. granzyme a (granzyme

254/292

1, cytotoxic t-lymphocyte-associated serine
esterase 3) (GZMA) gene.

```
<400> 402
tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttattttaa ctgctccctt gatagt cata attatccagt tgaggtgttt ctttgagaga 120
agaatataga caccaggccc acgagggctt ccgcatttat tttcaaggcc aaaggaagtg 180
accctcggga aaacaccctc gcacaacaaa gggcttcag aatctccatt gcacgagtct 240
cttcacctc ggaggcttcc agcacaaccc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgcactca 360
gagtatcggg acccaagatg cactattggt gagtcctgcc ccacctggc aacttggcac 420
atggttcctg gntttcacat caatccccct ttttagggag atgaaggata gtcacatatn 480
tggtnathtt ggctttttcc ggtcagctgt aaagttttaa ggtccc ctnc gcgtttggtg 540
gggcctagcc tgggagggga aanccttt 568
```

<210> 403

<211> 878

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic
t-lymphocyte-associated serine esterase 3) (GZMA)
gene.

<400> 403

```
cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtcgtttctc tcctgctaatt toctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactcctc attcaagacc ctacatgggc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttggtt agaaagagtt tcc ctatcca tgctatgacc 360
cagccacacg cgaaggtgac cttaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tacccttcat ctacctaaaa agggggatga tgtgaaacca ggaaccatgt 480
gccaagtgc agggtggggg aggactcaca atagtgcac ttgggtccgat actctgagag 540
aagtcaatat caccatcata g acagaaaag tctgcaatga tcgaaatcac tataatttta 600
accctgtgat tggaaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc cttttgttgt gcgaggggtgt tttccgaggg gtcacttct 720
ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctctcaa 780
agaaacacct caactggata attatgacta tcaagggagc agtttaaata accgtttcct 840
ttcatttact gtggcttctt aatcttttca caaataaa 878
```

<210> 404

<211> 191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(191)

<223> 3' terminal sequence. v-fos fbj murine

255/292

osteosarcoma viral oncogene homolog (FOS) gene.

<400> 404

```
gcagtgaccg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgccccctcgg 60
ccccctcgccc ggcttttgcta accgccacga t gatgtttctc gggcttcaac gcagactacg 120
aggcgctcatc ctcccgtgc agcagcgcggt ccccggccgg gataanctct ctttattaca 180
attaatcanc g 191
```

<210> 405

<211> 245

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(245)

<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 405

```
ttttcaactt aaatgctttt attgacaatg tcttgaaca ataagcaaac aatgcttaaa 60
tttttcattc aaattcactt tccacatgctc aaaagacctc aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacggt 180
ttcatggaaa actgttaatg tccngaacat tcagaccacc tcnacaatgn gtgntcngtn 240
anatt 245
```

<210> 406

<211> 489

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(489)

<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 406

```
gcgncgcgct caccgaaggg ngnangtaga cagcgggtca gaggccgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaatactt aggagacttg tt ttactcag agtggaatgt tttgccaggg acaaagtcaa 240
cacaagaaaa caaacaacaa aaaatagcca gaaagagaac agttaagtgc agctcgggtga 300
gtcccggcag ttccttcccg gcactggctc gtccctgggt tctcaagggt ccatgcccgc 360
acagcgtccg tccacctgtc cagcgcagcc acatgctgaa atgggagggt ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgcc a gagtagcttc gtctgaactt 480
gaacaagac 489
```

<210> 407

<211> 247

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(247)

<223> 5' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 407

```

tgttttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60
ctctggcatc tgcacatttc cgtgttacag cagctgcctg atgaa tttta tccacctcca 120
tttcagcatg tggctcgcgt ggacagggtg acggacgctg tggccgcatg gaaccttgag 180
aaccagga cgagccagt cgggaagga actgccggga ctcaccganc tgcncttaac 240
tgttctc 247

```

<210> 408

<211> 3059

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3059)

<223> interleukin enhancer binding factor 1 (ILF1)
gene.

<400> 408

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gtctgctcgc tcgcccggcg gctcgcgtc ggccccctcc ctcagctccg gtgcgcggcg 120
gccgacgacc cgcggccttg gctcggcgc gccaccggcg ccgcgcgga gcggcccggg 180
ggccctcacg caggcccatg gcggcgcgcg ggcgcgctct cgggcccggc accacgcggg 240
cgcgggggcg gggcgcgcg ggcggggggc ggtcccgccg ggcgctgggc cgtgggcgcg 300
ctggagggcc gcgagttcga gtatctgat aagaagcgt cggtgacct cggccgcaac 360
tcgtcgcagg gctcgggtga cgtgagcat ggccactcga gcttcattc ccggcgccac 420
ctcgagatct tcacgcccc ggcgggcgcg gccatggcg ggccgctccg gagctgccg 480
ccgcgcagcc caggcccagc gcggcgcgcg acttctacct gcgctgcttg ggcaagaacg 540
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agaagagaga gaagcaggag gcgtctgagt ctccagtga a ggccgtacag ccacacatct 720
cgcccctgac catcaacatt ccagacacca tggcccacct catcagccct ctgccctccc 780
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cctcgacctc ccagccaccc gtctgtcaga cgggtcacgt cgtccaccag atccagcgg 1620
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257/292

```

ctgtgggtcac cccggcagcc gtgctggccc ctctaagggc agaggcccag gagaatggag 1740
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gcaactgccag ccggatcatt cagacggcac agaccacccc ggtccagaag gtgaccatag 1860
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ctttgcacat gttggcaaca caogcatccg catcggcctc cctgcccaca aagcgccaca 2040
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cggcctcccg ccagcactcg ggggtgcagg gccctgtggt tggacttcac ctctcagcac 2280
tgaaaaccca aaaccagct ggcccttaaca ctccctaaag acagaagtca cacttgaaca 2340
aaaccacac acaacaaaac ctgatttggg agacggtgtc tccactgagc acctgctggg 2400
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gagtattttg aggtgtcctt tctttacaaa ataatgggt cttgggcatt tcacatcact 2640
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```

<210> 409

<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDI) gene.

<400> 409

```

tttttttttt tcttcagggt gcatttatatt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcctggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcacttggt cccttgtttg ttcttggtcg ggtcagggaa 180
ggcctgccgn ggggtggtggc a

```

<210> 410

<211> 297

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDI) gene.

<400> 410

258/292

```

ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60
gcttcaggag ggagcggana gccattctcc agggcccgctg gttgcccctg gacgtgtgcg 120
tctgctgctc cgggggtggan ctgggggtgtg ggatgcacgg cctcgtgggg gccggggccgt 180
cctccagccc cgctgctccc tggccagccc cc ttgtcgct gtcgggtccc tctaaccatg 240
atgccttaac atgtggagtg tacctgtggg gcctcactaa gcctctaant cactgtg 297

```

<210> 411
 <211> 1819
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1819)
 <223> rho gdp dissociation inhibitor (gdi) alpha
 (ARHGDI A) gene.

```

<400> 411
cctgaaccgc gcggccgaac cctccggtgt cccgaccag gctaagcttg agcatggctg 60
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actcgggtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180
aggacgacga gagcctgcga aagtacaagg aggcctgct gggccgcgtg gccgtttccg 240
cagaccccaa cgtccccaac gtgctggtga ctggcctgac cctggtgtgc agctcggccc 300
cgggccccct ggagctggac ctgacgggog acctggagag cttcaagaag cagtcgtttg 36 0
tgctgaagga ggggtgtggag taccggataa aaatctcttt ccgggttaac cgagagatag 420
tgtccggcat gaagtacatc cagcatacgt acaggaaagg cgtcaagatt gacaagactg 480
actacatggt aggcagctat gggccccggg ccgaggagta cgagttcctg acccccgtgg 540
aggaggcacc caagggtatg ctggcccggg gcagctacag catcaagtcc cgcttcacag 600
acgacgacaa gaccgaccac ctgtcctggg agtggaatct caccatcaag aaggactgga 660
aggactgagc ccagccagag gggggcaggg cagagtgatg gacggaagac ggacaggcgg 720
atgtgtcccc cccagcccc cccctcccca taccaagggt ctgagcaggc cctccgtgcc 780
cctccaccct ggtccgcct c cctggcctgg ctcaaccgag tgcctccgac cccctcctc 840
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tgtgtctgtg gggagagagg ccgagccag gcctctgctg ccctttctgt gccccccagg 960
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cctcactagc ctctactccc tgtgtctgca tgagc atgtg gcctccccgt cccttccccg 1260
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ccctcgatgg acaggcctga cccacccacc ctggggccag ccaggagccc cgcctgggcc 1560
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cagcctctca gtgccaccac ccccggcagc cttccctgac ccagccagg a caaacaaggg 1680
accaagtgca cacattgctg agagcogtct cctatagggt ccccgcccca tccccggtgt 1740
tggtgttgtg tctgccaggc tcaggcagag gcgcctgtcc ctgcttcttt tctgaccggg 1800
aaataaatgc ccctgaagg 1819

```

<210> 412
 <211> 306
 <212> DNA
 <213> Artificial Sequence

<220>

259/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(306)

<223> 3' terminal sequence. complement component
4a (C4A) gene.

<400> 412

```

gctgccaaaa gcctttaata tgccctgggtc ccaggctgt g ttcattgaaag cggacacagc 60
agtgtctcca gcttcatggg tcccagggttc aggttcctcc cagcggagggt gggaggggcag 120
ccctcacacc tggcaccctt gactgcatac tcctggagga agtcgttgag ctggggcacag 180
gctgcccgtc ggcgggttgcn tccggcacag gcgttcagag ggcattctct cgatccagct 240
attcgagtcc agcaagta ct nggggggggnc cctcccaggg gcataantng gncntccag 300
anccat                                     306

```

<210> 413

<211> 5417

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5417)

<223> complement component 4a (C4A) gene.

<400> 413

```

agaaggtagc agacagacag acggatctaa cctctcttgg atcctccagc catgaggctg 60
ctctgggggc tgatctgggc atccagcttc ttcaaccttat ctctgcagaa gccaggttg 120
ctcttgttct ctccttctgt ggttcatctg ggg gtcccc tatcgggtggg ggtgcagctc 180
caggatgtgc cccgaggaca ggtagtgaag ggatcagtg tctgagaaa cccatctcgt 240
aataatgtcc cctgtctccc aaagggtggac ttcacctta gctcagaaa agacttcgca 300
ctcctcagtc tccagggtgc cttgaaagat gcgaagagct gtggcctcca tcaactcctc 360
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acgacaaaca tccagggtat caacctgtct ttctcctctc gccgggggca cctctttttg 480
cagacggacc agcccattta caacctgtgc cagcgggttc ggtaccgggt ctttgctctg 540
gatcagaaga tgcgcccgag cactgacacc atcacagtca tgggtggagaa ctc tcacggc 600
ctccgcgtgc ggaagaagga ggtgtacatg ccctcgtcca tcttccagga tgactttgtg 660
atcccagaca tctcagagcc agggacctgg aagatctcag cccgattctc agatggcctg 720
gaatccaaca gcagcaccga gtttgagggtg aagaaatatg tccttcccaa ctttgagggtg 780
aagatcaccc ctggaaagcc ctacatcctg a cgggtgccag gccatcttga tgaaatgcag 840
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 ctgccctccc acctccgtg ggaggaacct gaacctggga accatgaagc tggagcact 5340
 gctgtgtccg ctttca tgaa cacagcctg gaccagggca tattaaggc ttttggcagc 5400
 aaagtgtcag tgttggc 5417

261/292

<210> 414
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(408)
<223> 3' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 414
ttacaatttt ccccaatagg tggcgcttct gaaacacagt atttgttttt atttttattt 60
tatttgagaa acccccaa at ttgctctgat ggcctttctt ctccatttgt catctctggg 120
aaccttgagt ctagatttag ggctgaaagt ctctctgcta ggagctttcc aaaatgcatt 180
gctttgattc tgggaactga ataggaggag aacacctgga ctactctgag tcctgagttc 240
aattctctct caactggttt ccttgaagggt ggctgtactg gtcactctct cgatccttga 300
ggggctggta gagctgggtca ttgggcaac a gagtctgctt gtctgnaagc tctcgactgg 360
gcgaactcca tcctgtccag caatgaagta gaccccaaag gcaaggac 408

<210> 415
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 415
aaccacttgg ttaagggtgta tgactatcaa gaagatgggt cggtacttct gacttgtgat 60
gcagaagcca aaaatatcac atggttttaa gatgggaaga tgatcggctt cctaactgaa 120
gataaaaaaa aatggaatct gggaagtaat gccaaggacc ctcgagggat gtatcagtgt 180
aaaggatcac agaacaagtc aaaaccactc caagtgtatt acagaatgtg tcagantctgc 240
attgaactaa atgcagccac catatctggc tttctctttg ctgaaatcgt cagcattttc 300
gtccttgctt ttgggggtcta cttcattgct ggacaggatg gag ttcgcca gtcgagagct 360
tcagacaagc agactctgtt gcccaatgac cagctctacc agcccctcaa ggatccgagg 420
aagatgacca gtacagccac cttcaagggg aaccagt 457

<210> 416
<211> 822
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

262/292

<222> (1)..(822)

<223> cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 416

```
gggctgctcc acgctttttgc cggagacaga gactgacatg gaacagggga agggcctggc 60
tgtcctcatc ctggctatca ttctttttca ag gtactttg gccagtgcaa tcaaaggaaa 120
ccacttggtt aagggtgatg actatcaaga agatgggtcg gtactttctga cttgtgatgc 180
agaagccaaa aatatcacat ggttttaaaga tgggaagatg atcggcttcc taactgaaga 240
taaaaaaaaa tggaatctgg gaagtaatgc caaggaccct cgagggatgt atcagtgtaa 300
aggatcacag aacaagtcaa aaccactcca agtgtattac agaatgtgtc agaactgcat 360
tgaactaaat gcagccacca tatctggctt tctctttgct gaaatcgtca gcatttttcgt 420
ccttgctggt ggggtctact tcattgctgg acaggatgga gttcgccagt cgagagcttc 480
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tgaccagtac agccaccttc aaggaaacca gttgaggagg aattgaactc aggactcaga 600
gtagtccagg tgtttctctc ctattcagtt ccagaaatca aagcaatgca ttttgaaag 660
ctcctagcag agagactttc agccctaaat ctagactcaa gggtcccaga gatgacaaat 720
ggagaagaaa ggccatcaga gcaaatttgg gggttttctc aataaaataa aaataaaaaac 780
aaatactgtg tttcagaagc gccacctatt ggggaaaatt gt 822
```

<210> 417

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 417

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acatctttat tgggaagact ctgaacaacc aacctacccc c caccttcaa gtctggggaa 60
ggnagggcag gantctgccc cctcctocca tatgtacaat cttttccgaa tcctactgga 120
gaaggtgccc ccacatgtgg aacagaggca gctgtaacaa gctagtgcac gggagccatg 180
tcccttttcc tctccggaact cagtttctct atctgtaaaa tgggctcaag gggaaacccg 240
tgcaacgagg cttctcgcca aggctganta tgtccacttc agaagcatga ggaagggcca 300
aggggatggg ggtgctagac atcctgggtt gggattgcac ggctcctcca cctccctccc 360
caccagtgcc cctcctcttg gcatcgcggg gctacgtggc ttcaggcccc gggataggag 420
gccgccccca aaggccgct 43 9
```

<210> 418

<211> 234

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(234)

<223> 5' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b

263/292

(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 418

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acgggggatg cccaacgtcc ttggggagct gaacagtctg gaccccatg gcatcgagag 60
caaacggcgg aagaaaaagc cggccatcct ggaccacttc ctgcccacc accggtcagg 120
cccgttcctc ccgccgtcag cctgtctgcc agaccctgac ttcttctctg ggcaccgtgt 180
tccttgcccc gcngggaggc cctggggggc ctgnacctcc tgggacgatg gggtt      234
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<210> 419

<211> 2314

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2314)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog b (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3) (RELB)
gene.

<400> 419

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ggaattcccc cccggccccg ccccgcgccc cgcagc cccg ggcgcccgc gtcctgcccc 60
gcctgcggcc cagcccttgc gccgctcgtc cgacccgcga tcgtccacca gaccgtgcct 120
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```

264/292

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cagacttgac ttgaaggTgg ggggtaggTt ggttgTtcag agtcttccca ataaagatga 2280
gtttttgagc ctcaaaaaaa aaaaaaggaa ttcc 2314
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<210> 420

<211> 214

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 420

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gagcatcccc ctggattctt tttcaaagt caaaagagggt ttacaagtgt gtttcattaa 120
acaaagcaaa gctgcgacaa aaccgagtca catcagtaat agtatgcatc ggcaaaaggg 180
catattaatc catcaaacac aatttgcat ttga 214
```

<210> 421

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 421

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atTTTgcact gtctTTTgag attcaagaaa aatttctatt cttttttttg catccaattg 240
tgctgaact tttaaaatat gtAAatgctg ccatgttcca aaccatcgt cagtgtgtgt 300
gtttagagct gtcaccctag aaaca acata ttgtcccatg agcaggtgcc tgagacacag 360
acccttttgc attcacagag aggtcattgg ttatagagac ttgaattaat aagtacatt 420
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cagtgtagag ctcttgTTTT atgggaaaag gctcaaatgc 520
```

<210> 422

<211> 6450

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(6450)
 <223> estrogen receptor 1 (ESR1) gene.

<400> 422

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aacgagctgg agcccctgaa ccgtccgcag ctcaagatcc ccctggagcg gccctgggc 480
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266/292

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```

<210> 423

<211> 580

<212> DNA

<213> Artificial Sequence

267/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(580)

<223> 3' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 423

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gaggcacagg ggcaggggaag atgacgaaaa ccaggctgac agctggaggc agggaaggggt 180
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```

<210> 424

<211> 503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(503)

<223> 5' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 424

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ctcgccctca actcccaact cggctggtgg atacccttcg ccatgttatc agccagacag 240
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gccccagttg ggcaggggca ggagggaggg tttctctccc aacgctgaag cggtcagact 480
ggaggtcaaa cgattaggca aac 503

```

<210> 425

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> pre-b-cell leukemia transcription factor 1
(PBX1) gene.

268/292

```

<400> 425
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```

<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli-kruppel family
member gli3 (greig cephalopolysyndactyly syndrome)
(GLI3) gene.

<400> 426

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cacatctcag ttaggtgaga tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaagtc agtttaatct cttcaactcc taatgatttc cgttggttgc agtctttttt 240
tcctaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgctg ggaatgggag 360
ggacgcccga gggctgggta aagccggaag aacctatgga aaaggtctca atgatacttg 420
ggctcagggc cccgacatca ggctcgagt gtcccatct ctatgattgc atcgaagtca 480
atctggtacc ctcccaggcc aggctg 506

```

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<210> 427
 <211> 239
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(239)
 <223> 5' terminal sequence. gli-kruppel family
 member gli3 (greig cephalopolysyndactyly syndr ome)
 (GLI3) gene.

<400> 427
 ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60
 tgtctctatt taaaaaacia aaagcctggt gtgggtgggtgc atgcctgtag tctcagcctc 120
 ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180
 agagacaggg tttcaccacg ttgccagagg cagtcttgaa ctctgacccc caagtgatc 239

<210> 428
 <211> 5054
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5054)
 <223> gli-kruppel family member gli3 (greig
 cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428
 cgatactacg tgggcatttt tggtcgaaga gagctgaagt aatgagaaga catcatggag 60
 gcccagctcc acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120
 tgtctcactc gaacagatgt gagcgagaaa gccgttgcc tccagcaccac ttctaattgag 180
 gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240
 cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300
 gcctcattga tcaagaaaga gatccatggg tccctggcac acgtggcgga gccctctgtg 360
 ccgtaccgcg ggacggtg tt tgccatggac cccaggaatg gttacatgga gcccactac 420
 caccctcctc atcttttccc tgccttccat cctcctgtac caattgatgc cagacatcat 480
 gagggcggtt accattacga tccatctccg attctc
 cat tgcatatgac ttccgcctta 540
 tctagtagcc ctacgtatcc ggacctgcc ttcattagga tctccccaca ccggaacc cc 600
 gctgctgctt ccgagtctcc ctccagccct ccacatccct acattaatcc ctacatggac 660
 tatatccgct ccttgacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720
 agccctacag atgcgcccc tgcaggagtc agccagcag aatactatca tcagatggcc 780
 ctgctaactg gccagcgcag cccctatgca gacatt attc cctcagctgc caccgcccgc 840
 acggggggcca tccacatgga atatcttcat gctatggata gcaccagatt ctccagcccc 900
 aggctgtcag ccaggccgag ccgaaaacgt acaactgtcca tatcaccact ctccgatcat 960
 agctttgacc ttcagaccat gataaggacg tctcccaact ccttggtcac gattctcaat 1020
 aattcccgtg gca gctcttc agcaagtggc tccatagggtc acttatctgc aagtgaatc 1080
 agccctgcct tgagcttcac ctactcttcc gcgcctgtct ctctccacat gcatcagcag 1140
 atcctaagcc gacaacagag cttaggttca gcccttggac acagccctcc actcatccac 1200
 cctgccccaa cttttccaac acagaggcct attccaggga tccctacggt tc tgaacccc 1260

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gtccagggtca	gctccggccc	ttctgagttcc	tcacagaaca	agccccacgag	tgagtctgca	1320
gtgagcagca	ctggtgaccc	gatgcacaac	aagagggtcca	agatcaaaacc	cgatgaagac	1380
ctccccagcc	caggggctcg	ggggcagcag	gaacagccccg	aaggaacaac	ccttgtcaag	1440
gaggaagggg	acaaagatga	aagcaaa cag	gagcctgaag	tcattctatga	gacaaaactgc	1500
actggggaag	gctgcgcgag	ggagtctcgac	acccaagagc	agcttggtgca	ccatataaat	1560
aacgaccata	ttcatggaga	gaagaaggag	ttcgtgtgca	gggtggctgga	ctgctcaaga	1620
gagcagaaac	ccttcaaagc	ccagtatatg	ttggtagtgc	atatgagaag	acacacgggc	1680
gagaagcctc	acaaatgcac	ttttgaagggt	tgcacaaagg	cctactcgag	actagaaaac	1740
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tgcaacaagg	ctttctcaaa	tgctcttgat	cgcgcacaaac	acaaaaacag	aacgcattcc	1860
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tccctccgga	aacatgtgaa	gacagtgcac	ggcccagagg	ctcatgtcac	caagaagcag	1980
cgaggggaca	tccatcctcg	gccgccaccc	cagagagatt	ccggcagcca	ttcacagtcc	2040
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gccatcgatg	aaaccccaat	catggactca	accattttcca	ctgcaaccac	agcc cttgct	2340
ttgcaagcca	ggagaaaccc	ggcagggacc	aatggatgg	agcacgtaaa	actagaaagg	2400
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gcggtctctc	ctctcatagg	aaatggcaca	cagtccaaca	acacctgcag	cttgggtggg	2520
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atgtcaaca	gaagggacag	cagcgccagc	accatcagct	cggcctacct	gagcagccgc	2640
cgtccttcag	ggatctcgcc	ctgcttctcc	agcgcgcgt	ccagcgaggc	gtcacaggcc	2700
gagggccggc	cgcagaacgt	gagcgtggcc	gactcctacg	accccatctc	caccgacgcc	2760
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ggagcccacg	gctacggggc	gcgccacctg	cagccgcacg	atgcgctggg	ccacggcgctg	3060
aggagggcca	gcgaccgggt	gcggacaggc	tccgagggcc	tggccctgcc	tcgtgtgccg	3120
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cagaaccaag	cagggtagca	gcagcacttc	cccagcgccc	tcccggacga	cagcaa agtg	3420
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ttccatgccc	tcgagcagcc	ctgcccgcag	ggcagcaaaa	ccgacctgcc	cattcagtgg	3540
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cccgtgtgc	cgcagactgc	cgccttttggg	ttctgcaacg	gcattggtcgt	ccaccgcgag	3660
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tacggtggcc	cagagcactt	gatgtctccac	aacagccccg	gaagtggcac	cagtggaaac	3780
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gagtcagctg	gcagcatggt	gaatggcatg	cagaaccagg	acccagtggg	acaggggtac	4020
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taccagccat	gtgccagctt	tgggggcagc	aggcgcagg	ctatgccgag	ggacagcctt	4260
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ttctatgacc	aaaccgtggg	cttcagtcag	caagacacga	aagctgggtc	attctctatt	4440
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gggtgctaate	aggtgacaag	cacagtggac	agcctcgaca	gccatgacct	ggaaggggta	4560
cagattgact	tcgatgccat	catagacgat	ggggaccact	ccagcctgat	gtcggggggc	4620
ctgagcccaa	gtatcattca	gaacctttcc	catagctcct	ccgcctcac	cacgcctcgg	4680
gcgtcccttc	cattcccagc	gctgtccatg	ag caccacca	acatggctat	cggggacatg	4740
agttcttttc	tgacctccct	agcggaagaa	agcaaatctc	ttgcagttat	gcaataggct	4800
ttaggtaaaa	aagactgcaa	ccaacggaaa	tcaataggag	ttgaagagat	taaaactgact	4860
ttgttttggc	tgttttttta	gttctgtatg	tatttttagca	atctcatctc	acctaaactga	4920

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gatgtgtttc aattatattc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980
agggagaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040
tttttaaaaa aaaa 5054

<210> 429
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(271)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 429
aggagacttg ttttactcag agtggaaaaat tttgccaggg acaaagtc aa cacaaagaaa 60
caaacaacaa aaaatagcca gaaagagaac agttaagtgc agctcgggtga gtcccggcag 120
ttccttcccg gcactggctc gtccctgggt tctcaagggt ccatgcggcc acagcgtccg 180
tccacctgtc cagcgcagcc acatgctgaa atggagggtg ataaaattca tcaggcagct 240
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430
<211> 193
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(193)
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,
sw|Q08999|RBL2_HUMAN.

<400> 430
TGTCTACATT TNCCACATA AAAATGAAAC AATNNTTCT CTCGNGAAA AGATTTTATA 60
TACTTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNNGAT GGCNGTGAAT NCACTGCAAA 180
NAGCATTTGC CCN 193

<210> 431
<211> 184
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(184)
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).

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<400> 431
AGTCAAAGCT TTTATTTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGGCAC 60
ATAAGAAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120
AATCACTTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180
TCTG 184

<210> 432
<211> 242
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(242)
<223> 5' terminal sequence. Similar to NM_022641 Homo sapiens
chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1

<400> 432
ATTTCGGCAG ATGACTGGCC AGGGTATAAA AAGGGCCCCAC AAGAGACCGG CTCTAGGATC 60
CCAAGGCCCA ACTCCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180
AANAAGCTNG TGCCNTCCAA ANCGTTCCGT TATCCAGGGT TTTTGACCAC GCTATGCTNC 240
AA 242

<210> 433
<211> 329
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(329)
<223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433
AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60
CTTGACAGAC GCCTGCCAGG GNATTTCTGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC GACCGTGACC 240
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300
GCAAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434
<211> 247
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

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<222> (1)..(247)

<223> 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 434

```
AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG                                         247
```

<210> 435

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(63)

<223> 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 435

```
CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGGAG CTGCTGTGGC 60
TTT                                         63
```

<210> 436

<211> 190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(190)

<223> 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 436

```
GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCACTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG                                         190
```

<210> 437

<211> 176

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(176)

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

```
CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTNN TTGCACCTGC 60
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176
```

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P, granule membrane protein CD62, SELP

<400> 438

```
NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60
TTTTCTGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120
TACACTGGAC TTAACATAAA TGCATTTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240
CTGTTTCCTG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300
GTCCACCTC TTCTCTTCCT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTTCTGCA 360
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465
```

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P, granule membrane protein CD62, SELP

<400> 439

```
GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60
TGGGGGCAGG AAGGCCACAG GNGACATGTG GCCTTCTAGC TTNATNCTTG GCCTTCTGCA 120
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCTC 180
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360
TGGTATTTCA AGTAACAGGT GAGNNAAGG ANAGAG 39 6
```

<210> 440

<211> 337

<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(337)

<223> 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 440

```
AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTTCCCT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTCTTGA GCTGCAGCTG GCGGGTAGGG CNCGGGGCCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCA CAGGNGT 337
```

<210> 441

<211> 104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prim er

<220>

<221> misc_feature

<222> (1)..(104)

<223> 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 441

```
TTCCCGCCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGGNAAAN AGTTTNTGAA NCACCAGAAA CCTT 104
```

<210> 442

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(223)

<223> 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

<400> 442

```
AAGCAATGGA TGATTTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGGCNGCC CCTGCACCAG CCCCCTCCTG GCCCCTGTCA TCTTCTGTCC 180
CTTCCCAGAN AACCTACCAG GGCAGCTACG GTTTCCTCT G GG 223
```

<210> 443

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<211> 223
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> 5' terminal sequence. Tumor protein p53
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60
caggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tcttctgtcc 180
cttccagan aacctaccag ggcagctacg gtttccgtct ggg

<210> 444
<211> 343
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(343)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(343)
<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 444
caaggggctg caaactnncc cacacatgac cccagccctc tacagcggta cagtgaggac 60
cccacagtac ccttgccctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cggccccagc ccccttcgcc ccgagaggcc 180
ctctgcctgc tgcccgacct gctggtgcca ctctggaaag gccaagact ctctccccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc cttt gggggt gccgtgggag aacccccgagt 300
attgacaccc caggggaggg agcttgccct tcagccccac ctt 343

<210> 445
<211> 309
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(309)
<223> 3' terminal séquence.

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<220>
<221> misc_feature
<222> (1)..(309)
<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagaggtgg aaaaaagggc 60
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tccctggcct 120
caagttaagg ggggcacggg agcgccnttg acagtcattt tgcgccccct gctggtngaa 180
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc cccacttgct 240
ntcgaagggg ganttgggna ngtagggtn gtngettgan gcccatngga actnggaaaa 300
ccatnggat 309

<210> 446
<211> 268
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(268)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(268)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 446
attatcttgt gaatctactt agaaaaacac acacaagcaa tggtcacaac tataaattta 60
aaccttttgc actaaaaaaaa caaaaaaca caaacacaan accacaggca tgaactgtaa 120
acctgtatta actntgaact ggtcttaagg ttaattctta gcngtcattc agtattttcc 180
tccttggaac ctgtaatgtt ttngcacggg ntgatctccc gcnggggggta ctagtaatga 240
ctggctgccc gtgtagggag atgcttcc 268

<210> 447
<211> 169
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(169)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(169)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 447

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gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60
atgaaattaa agtctgagga cgagagcacg nctgggngcg aaantntgcc tttttntac 120
ggatgcacta cantaaagan gtgcanccta tncgncccct gccctactt 169

<210> 448
<211> 393
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(393)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(393)
<223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

<400> 448
aagtaattaa gggtagttaa attattttaa gtatacaaag tccaaacagc caggggtaag 60
gtctccaaga ggccttccca gggtaagga gagggccaca agggaacctt ggagtttgaa 120
agacaaaggg aacacatgac atcaaagtgc aggctagaaa tttcacttag aagaaaataa 1 80
cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgctg 300
aacttactat gttaactatg atagtgtgtc tacnatagat atcncgatgg ttaaaagctg 360
gtaaaaggta atggttctca aaaccnaaa a tag 393

<210> 449
<211> 217
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(217)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(217)
<223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

<400> 449
ttacctggt atctcctact gtagtatgag gaagaatggc tgtaaatgta ttttttgaat 60
tctggnctca cctttgtctc agctaaatgt agccgcatcc gggacacagt ttgtgccaca 120
tgtgccgaga attcctacaa cgagc actgg aactacctga ccatctgccca nctgtgccgc 180
ccctgtgacc cagtgatggg cctcgnctga gantgcc 217

<210> 450
<211> 157
<212> ADN

279/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(157)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(157)

<223> (POU2F2) gene.

<400> 450

```
nattcggcaa cgnggaaagg aaagaaacta accaacaaaa gagaaaacca aaaataatca 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gaccaaaaaa acaacca                               157
```

<210> 451

<211> 282

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(282)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(282)

<223> caspase 4, apoptosis -related cysteine protease
(CASP4) (ex CASP1)

<400> 451

```
gagaatctga cagccagga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtcct ctgacagcac attcttggtc ctcatgtctc atggcatcct ggagggaatc 120
tgcggaactg tgcgatgatg gaaaaaacca gatgtgctgc tttatgacac catcttccag 180
atattcaaca accgcaactt gcctcagtct ngaaggacaa acccaaggtc atcattgtnc 240
agggcttgca gagggtgcaa accttggggg aantttgggg tc                               282
```

<210> 452

<211> 424

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(424)

<223> 5' terminal sequence

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<220>
<221> misc_feature
<222> (1)..(424)
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452
ttgcttttng caaaactcta cttaatccaa tnggtttttc cctgtacagt agattttcca 60
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgcct 120
ctgtgctgtg tgtgacgtga ccggactttt ctgcaaacac caacatgttg ggaaacttgg 180
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctggttcc agggtccttc 240
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300
gttttataag ggctgatgtc aatttinctgt gtttgccaan ttccaagccc catcttncta 360
aatgggcaaa aggaaggtgg gatgggcccc agcnacagct ttgnaccc ga gggctnttgg 420
gtca 424

<210> 453
<211> 435
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(435)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(435)
<223> Itegrin, beta 2 (antigen CD18 (p95), lymphocyte
function-associated antigen 1; macrophage antigen
1 (mac-1) beta subunit) (ITGB2)

<400> 453
aggagtgcgc cggctgcccc tcaccctgtg gcaagtacat ctctgcgcgc gaggtcctga 60
agttcgaaaa gggcccctnt ggaagaactg cagcgcgggc tgtccggggc tgcagctgtc 120
gaacaacccc gtgaagggca ggacctgcaa ggagagggac tcagagggct gctgggtggc 180
ctacacgctg gaggcagcagg acgggatgga ccgctacctc atctatgttg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctcctg ctggatcatc gggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agnaggagaa gctcaagtcc cagtnggaac aatgattatt 420
ccctttttca agagc 435

<210> 454
<211> 544
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(544)

281/292

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)

<400> 454

```
gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgnc aagcagnacg 60
nctnacaaca tcaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggacgt aaaagatott ctgnctgncc acggaggcct gttccccgga 180
cctgncagtt ctatggnagc agattcggcg ggatcatgcg gccacacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggctggg 300
gcgagaacga ccgtgggcgt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttggaact catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgcc aagcgcantt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgcatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn 544
```

<210> 455

<211> 344

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)

<400> 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cagcaggaac 60
cggcgggcggc gngtgcngt agggccgtg n gcggtgncgg cgcgggagga gccggannca 120
gccggcnggg gcggngggca ncanggacga gaaggngnnc accaaggagc tggaccagng 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagncc caggncaga gccncagcga 240
gaangcnaaa gaaanccnga caaaagaanc caacngcaa gaggnncgan gnccagnnac 30 0
ngnccngnga gangngcang ggcaannnca ngaacccatg gaac 344
```

<210> 456

<211> 514

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(514)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(514)
<223> S100 calcium-binding protein A11 (calgizzarin)
(S100A11)

<400> 456
cagcctcccc cgctcgcgc agctccaaca tggcaaaaat ctccagccct acagagactg 60
agcgggtgcat cgagtccctg attgctgtct tccagaagta tgctggaa ag gatgggttata 120
actacactct ctccaagaca gagttcctaa gcttcatgaa tacagaacta gctgccttca 180
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240
gtgatggta gctagatttc tcagaatttc ttaatctgat tgggtggccta gctatggctt 300
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggacccctt 360
gggcccctggg cctttcaaac ccacccctn ttccctttcca gcctttctgt tcatcatntt 420
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtn ccaactggtc 480
attagttatt aaaggnaatg tnaatttttt ttaa 514

<210> 457
<211> 359
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(359)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(359)
<223> Granzyme A (granzyme 1, cytotoxic
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457
gctggacgtc atcaacaagc attcattcaa caacttccgc ctgcgagtgg ggttgaacca 60
tggaaccgta gtagctggag ttattggggc ccagaagccg caatatgaca ttgggggcaa 120
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgaac 180
tgaggagaca gcatggggcc tacagtccct gggctacacc tgctacagcc nggggtgtca 240
tcanggtgaa aggcaaaggg cagctctgca cctacttctt gaacacagac ttgacacgaa 300
ctggacctcc ttcagctacc ctaggctgag attgcactcg cct tncctaag aacctnaat 359

<210> 458
<211> 1251
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1251)
<223> 3' terminal sequence

<220>

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<221> misc_feature
<222> (1)..(1251)
<223> endothelin 1 (EDN1)

<400> 458

```
ggagctgttt accccactc taataggggt tcaatataaa aagcggcag agagctgtcc 60
aagtcagacg cgcctctgca tctgcgccag gcgaacgggt cctgcgcctc ctgcagtcac 120
agctctccac caccgcgcg tgccgctgca gacgctccgc tcgctgcctt ctctcctggc 180
aggcgtgtcc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaaccgc agcgctttga gggacctgaa gctgtttttc ttcgttttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttccagaatgg attatttgct catgattttc 360
tctctgctgt ttgtggcttg ccaaggagct cc agaaacag cagtcttagg cgctgagctc 420
agcgcggtgg gtgagaacgg cggggagaaa cccactccca gtccaccctg gcggctccgc 480
cggctccaagc gctgctcctg ctgctccctg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccgag cacgttggtc cgtatggact tggaagccct 600
aggtccaaga gagccttggg gaatttactt ccacaaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgotggaatt tttgccaagc agggaaaagaa 720
ctcagggtgt aagacattat ggagaaagac tgggaataatc ataagaaagg aaaagactgt 780
tccaagcttg ggaaaaagtg tatttatcag cag ttagtga gaggaagaaa aatcagaaga 840
agttcagagg aacacctaag acaaaccagg tcggagacca tgagaaacag cgtcaaatca 900
tcttttcatg atcccaagct gaaaggcaag ccctccagag agcgttatgt gaccacacaac 960
cgagcacatt ggtgacagac ttcggggcct gtctgaagcc atagcctcca cggagagccc 1020
tgtggccgac tctgcactct ccacctgtgc tgggatcaga gcaggagcat cctctgctgg 1080
ttcctgactg gcaaaggacc agcgtcctcg ttcaaaacat tccaagaaag gttaaggagt 1140
tcccccaacc atcttcactg gcttccatca gtggtaactg ctttggtctc ttctttcatc 1200
tggggatgac aatggacctc tcagcagaaa caca cagtca cattcgaatt c 1251
```

<210> 459
<211> 2145
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2145)
<223> 3' terminal séquence

<220>
<221> misc_feature
<222> (1)..(2145)
<223> Protein tyrosine phosphatase, non -receptor type 6
(PTPN6)

<400> 459

```
cggcagaact gggaccaccg ggggtggtga ggcgcccg cactgggagc tgcactgtag 60
gcttagtccc tgagctctct gcctgccag actagctgca cctcctcatt ccctgcgccc 120
ccttcctctc cggaa gcccc caggatgggt aggtggtttc accgagacct cagtgggctg 180
gatgcagaga ccctgctcaa gggccgaggt gtccacggta gcttcctggc tcggcccagt 240
cgcaagaacc agggtgactt ctgctctccc gtcagggtgg gggatcaggt gaccatatt 300
cggatccaga actcagggga tttctatgac ctgtatggag gggagaagt t tgcgactctg 360
acagagctgg tggagtacta cactcagcag cagggtgtgg tgcaggaccg cgacggcacc 420
atcatccacc tcaagtaccc gctgaactgc tccgatecca ctagtgagag gtggtacat 480
ggccacatgt ctggcgggca ggcagagacg ctgctgcagg ccaagggcga gccctggacg 540
tttcttgtgc gtgaga gcct cagccagcct ggagacttcg tgctttctgt gctcagtgc 600
cagcccaagg ctggcccagg ctcccgcctc agggtcaccc acatcaaggt catgtgcgag 660
ggtggacgct acacagtggg tggtttggag accttcgaca gcctcacgga cctggtggag 720
```

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```

catttcaaga agacgggggat tgaggaggcc tcaggcgcct ttgtctacct gcggcagccg 780
tactatgcc aagcaggagt cagaggatag agccaaggct ggcttctggg aggagtttga gagtttgcag 840
aagcaggagt cgaagagctt gacaccagct ctggaagggc aacggccaga gaacaagggc 960
aagaaccgct acaagaa cat tctccccctt gaccacagcc gagtgatcct gcagggacgg 1020
gacagtaaca tccccgggtc cgactacatc aatgccaaact acatcaagaa ccagctgcta 1080
ggccctgatg agaacgctaa gacctacatc gccagccagg gctgtctgga ggccacggtc 1140
aatgacttct ggcagatggc gtggcaggag aacagccgtg tcatcgtcat gaccacccga 1200
gaggtggaga aaggccggaa caaatgcgtc ccatactggc ccgaggtggg catgcagcgt 1260
gcttatgggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
cagtacctga gctggccc ga ccatgggggtc cccagtgagc ctgggggtgt cctcagcttc 1440
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tgcagcgccg gcatcgcccg cacaggcacc atcattgtca tcgacatgct catggagaac 1560
atctccacca agggcctgga ctgtgacatt gacatccaga agaccatcca g atggtgcgg 1620
gcgcagcgct cgggcctggt gcagacggag gcgcagtaca agttcatcta cgtggccatc 1680
gcccagttca ttgaaaccac taagaagaag ctggaggtcc tgcagtcgca gaagggccag 1740
gagtcggagt acgggaacat cacctatccc ccagccatga agaatgccc tgccaaggcc 1800
tccccgacct cgtccaaac a caaggaggat gtgtatgaga acctgcacac taagaacaag 1860
agggaggaga aagtgaagaa gcagcgggtc gcagacaagg agaagagcaa gggttccctc 1920
aagaggaaagt gagcgggtgct gtcctcaggt ggccatgcct cagccctgac cctgtggaag 1980
catttcgcga tggacagact cacaacctga acctaggagt gccccattct tt tgtaattt 2040
aaatggctgc atccccccca cctctccctg accctgtata tagcccagcc agggcccagg 2100
cagggccaac ccttctcctc ttgtaataaa agccctggga tcaact 2145

```

<210> 460

<211> 2149

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2149)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(2149)

<223> Transcription factor AP -4 (activating enhancer binding protein 4) (TFAP4)

<400> 460

```

gacctgcaaa cacacacac a cacacacaca cacacacaca cacacacaca catacacacg 60
caccagggga gccgagagac ctccctcccg cccctcccat gccgcctcc ctccctcgc 120
cgccgccgccc gccgccagca tctgggaccg gccgattctg caccctcgtc cggcgctgcc 180
ctttgattcg gatttccatc ttgcattctc cggctgatcg cgggacctgg ct cgtgcaga 240
ggaggggggc cgatcgctat ggagtatttc atggtgccc ctcagaagggt gccctctttg 300
caacatttca ggaaaacaga gaaagaagtg ataggagggc tctgtagcct tgccaacatt 360
ccactaacc cagagactca gcgggaccag gagcgggcga ttcggcggga gatcgccaac 420
agcaacgagc ggagacgcat gcagagcatc aacgcgggat tccagtcctt caagaccctc 480
atccccaca cagacggaga gaagctcagc aaggcagcca ttctccagca gacagccgag 540
tacatcttct ccctggagca ggagaagacc aggtctttgc agcagaacac acagctcaag 600
cgcttcatcc aggagctgag cggctcgtcc cccaagcgac ggcgggcaga gga caaggac 660
gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgggag 720
atgattgagc tgcggcagca gctggacaag gagcgctcgg tgcgcatgat gctggaggag 780
caggtgcgct cgctggaggc ccacatgtac ccggaaaagc tcaagggtgat tgcgcagcag 840

```

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```

gtgcagctgc agcagcagca ggaacaggtg aggctgctgc accaggagaa gctggagcgg 900
gaacagcagc agctgcgga cagcttctg cccctccgg ccccccacca ccacccacg 960
gtgatcgtgc cagcaccgcc tctctctccc tcccaccaca tcaatgtcgt caccatgggc 1020
ccctcctcgg tcatcaactc tgtttccaca tcccggcaaa atctggacac catc gtgcag 1080
gcaatccagc acatcgaggg caccagga aagcaggagc tggaggagga gcagcggcga 1140
gctgtcatcg tgaagcctgt ccgcagctgc ccggaggccc ccacctctga caccgcctcc 1200
gactccgagg cctcagacag tgacgccatg gaccagagcc gggaggagcc gtcgggggac 1260
ggggagcttc cctgactacc c cccagccc tctctctcct tctgggggct ggaggagacc 1320
ggggcagcca caggagagaa catgggcgaa tgagtgcgaa atttttacaa aattacgatg 1380
tcatttgggt ctcttttatg acctcttttt caatactgta aatcgaccct tgaacgaagc 1440
cactcaaccc gaggtcccgg ggctgggggtg tcgcagagct gtgggagcat cggca ccca 1500
gggcggggcc tcggcccgcc gggtggagg aagctgacac ggagatgcct ggcctctctc 1560
tgccaaaaag cattttttcc ttttaatatg ttttttaaga acagggaaaa ttaacaaaaa 1620
cccaggtta tttcttccct gccagagcc agcctgggat tgtcagcctt caatcccctt 1680
tccttctctt ttttgggttt tc tcttttct cttttaagca cttacatggt tgggggtaag 1740
actaggctgg ggcattctgg gggcccgag gtctccgtt cttcttggtt ggggtttgct 1800
gctgctgtgc cccctcccc cttcccatc tcggcactag aattcgccac tctccaccc 1860
cccagcccc acctctgct ccaggtctca tcttccacc caaaaatgtc tgtctc tctc 1920
tttttgtttt gtttgttgtt ggttttttat ttcttttttg tttgctttct gtttttgttt 1980
tgtttttctt ttttttcttt cttttttttt tttttacaat tttgaggtct tcgtgttcaa 2040
ggagaagcta ttatattttg ttaagaaagt ggggagaaaa aaaaccaaga ggccaccgtg 2100
cctttgtaaa gaaacaaaat aaa gtttgta ctttggtttt taaaaaaaaa 2149

```

<210> 461

<211> 6478

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6478)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(6478)

<223> Cyclin D2 (CCND2)

<400> 461

```

agagcgagca ggggagagcg agaccagttt taaggggagg accggtgcga gtaaggcagc 60
cccagggtct tgctcgccca ccacccaato ctgcctccc ttctgctcca ctttctctt 120
ctgccctcac ctctcccccg aaaacccctt atttagccaa aggaagg agg tcagggggaa 180
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<210> 462

<211> 3490

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3490)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(3490)

<223> Junction plakoglobin (JUP)

<400> 462

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cctacgactc gggatatccac tcgggcgcga acacctgcgt gccctccgtc agcagcaagg 240
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<210> 463

<211> 1355

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1355)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1355)
<223> Growth arrest and DNA -damage-inducible, alpha
(GADD45A)

<400> 463
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<210> 464
<211> 732
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(732)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(732)
<223> Non-metastatic cells 1, protein (NM23A) expressed
in (NME1)

<400> 464
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gttgacctga aggaccgtcc attctttgcc ggccgtgtga aatacatgca ctcaggggccg 300

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tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720
cttcctccca gc

<210> 465

<211> 942

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(942)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(942)

<223> Ribosomal protein L13 (RPL13) (ex BBC1)

<400> 465

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<210> 466

<211> 755

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(755)

<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(755)
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466
caccatgagc cctctgctcc gccgcctgct gctcgccgca ctctctgcagc tggccccccgc 60
ccaggccccc gtctcccagc ctgatgcccc tggccaccag aggaaagtgg tgtcatggat 120
agatgtgtat actcgcgcta cctgccagcc ccgggaggtg gtggtgccct tgactgtgga 180
gctcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240
tggctgctgc cctgacgatg gcctggagtg tgtgcccact gggcagcacc aagtccgga 300
gcagatcctc atgatccggt acccgagcag t cagctgggg gagatgtccc tggaagaaca 360
cagccagtgat gaatgcagac ctaaaaaaaaaa ggacagtgct gtgaagccag acagggctgc 420
cactccccac caccgtcccc agccccgttc tgttccgggc tgggactctg cccccggagc 480
accctcccca gctgacatca cccatccac tccagcccca ggccccctctg cccacgctgc 540
acccagcacc accagcgccc tgacccccgg acctgccgcc gccgtgccg acgccgcagc 600
ttcctccgtt gccaagggcg gggcttagag ctcaaccag acacctgcag gtgccggaag 660
ctgcgaaggt gacacatggc ttttcagact cagcaggggtg acttgccctca gaggctatat 720
cccagtgggg gaacaaagag gagcctggta aa aaa 755

<210> 467
<211> 1039
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1039)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1039)
<223> Laminin receptor 1 (67kD, ribosomal protein SA)
(LAMR1)

<400> 467
tgccctgtctt ttccgtgcta cctgcagagg ggtccatacg gcgttggttct ggattcccgt 60
cgtaacttaa agggaaactt tcacaatgtc cggagccctt gatgtcctgc aaatgaagga 120
ggaggatgtc cttaa gttcc ttgcagcagg aaccactta ggtggcacca atcttgactt 180
ccagatggaa cagtacatct ataaaaggaa aagtgatggc atctatatca taaatctcaa 240
gaggacctgg gagaagcttc tgctggcagc tcgtgcaatt gttgccattg aaaacctgc 300
tgatgtcagt gttatatcct ccaggaatac tggccagagg gctgtgctg a agtttgctgc 360
tgccactgga gccactccaa ttgctggccg ctctactcct ggaaccttca ctaaccagat 420
ccaggcagcc ttccgggagc cagggtttct tgtggttact gaccccaggg ctgaccacca 480
gcctctcacg gaggcattct atgttaacct acctaccatt gcgctgtgta acacagattc 540
tcctctgcgc tatgtg gaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600
tttaatgtgg tggatgctgg ctcggaagt tctgcgcatg cgtggcacca tttcccgtga 660
acacccatgg gaggtcatgc ctgatctgta cttctacaga gatcctgaag agattgaaaa 720
agaagagcag gctgctgctg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780
tgctcccgtc cctgagttca ctgctactca gcctgaggtt gcagactggt ctgaaggtgt 840
acaggtgccc ttgttgccca ttcagcaatt cctactgaa gactggagcg ctcagcctgc 900
cacggaagac tggctctgag ctcccactgc tcaggccact gaatgggtag gagcaaccac 960
tgactgggtc taagctg ttc ttgcataggc tcttaagcag catggaaaaa tgggttgatgg 1020
aaaataaaca tcagtttct 1039

<210> 468
<211> 240
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(240)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(240)
<223> Chorionic somatomammotropin hormone 1 (placental
lactogen) = LACTOGEN Precursor

<400> 468
attcggcacg atgactggcc agggataaaa aagggccac aagagac cgg ctctaggatc 60
ccaaggccca actccccgaa ccactcaggg tcctgtggca gtcacctag tggcaatggc 120
tccaggctcc cggaacgtcc ctgatacctg nttttgncct nctctnactg ccctggnttn 180
aanaagctng tgccntccaa ancgttcctg tatccagggt ttttgaccac gctatgctnc 240